

105 18 33.3 492 1 TISD HUMAN
 106 18 33.3 507 1 PGL2_JUNAS
 107 18 33.3 514 1 PGL2_CHA0B
 108 18 33.3 514 1 PGL2_CRYJA
 109 18 33.3 514 2 Q8H987
 110 18 33.3 514 2 Q8H988
 111 18 33.3 514 2 Q8H989
 112 18 33.3 516 2 Q8AR84
 113 18 33.3 522 2 Q8CBL5
 114 18 33.3 523 2 Q8BQEL
 115 18 33.3 525 1 MP11 RAT
 116 18 33.3 555 2 Q8H139
 117 18 33.3 584 1 COB8 HUMAN
 118 18 33.3 632 2 Q7K6U7
 119 18 33.3 634 2 Q91LA5
 120 18 33.3 660 2 Q7QY47
 121 18 33.3 667 2 Q9XTK3
 122 18 33.3 671 2 Q9D678
 123 18 33.3 675 1 KSC5 ECOLI
 124 18 33.3 675 2 Q6KD00
 125 18 33.3 675 2 Q8FDP9
 126 18 33.3 690 2 Q7QE14
 127 18 33.3 698 2 Q9D2L6
 128 18 33.3 742 2 Q9N8X0
 129 18 33.3 746 2 Q27526
 130 18 33.3 750 2 P70921
 131 18 33.3 762 2 Q7YVQ5
 132 18 33.3 762 2 Q9E293
 133 18 33.3 763 2 Q89K15
 134 18 33.3 798 2 Q8C7A1
 135 18 33.3 822 2 Q9V9C6
 136 18 33.3 827 2 Q6TDN9
 137 18 33.3 827 2 Q6TDP0
 138 18 33.3 827 2 Q8CFM7
 139 18 33.3 838 2 Q8R3S1
 140 18 33.3 839 2 Q7R186
 141 18 33.3 888 2 Q6KAT0
 142 18 33.3 891 2 Q6TDN6
 143 18 33.3 908 2 Q8OYR4
 144 18 33.3 914 2 Q8CFM8
 145 18 33.3 923 2 Q6TDN8
 146 18 33.3 1015 2 Q6TDN7
 147 18 33.3 1027 2 Q9FGS8
 148 18 33.3 1046 2 Q6L2Q9
 149 18 33.3 1048 2 Q05925
 150 18 33.3 1144 2 Q6H8C5

ALIGNMENTS

RESULT 1
 YA40_MYCPN STANDARD; PRT; 103 AA.
 AC P75074;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein MPN040 (B01_orf103b).
 GN OrderedLocusNames=MPN040; ORFNames=MP114;
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
 RA Himmelreich R., Hilbert H., Plegens H., Firkel E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae";
 RL Nucleic Acids Res. 24:4420-4449(1996).

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 CC -----

DR EMBL; AE000014; AAB95762.1; -.
 DR PIR; S73440; S73440.
 KW Complete protosome; Hypothetical protein.
 SQ SEQUENCE 103 AA; 11291 MW; 62B9684733993C6 CRC64;

Query Match 35.2%; Score 19; DB 1; Length 103;
 Best Local Similarity 13.6%; Pred. No. 6.2e+02;
 Matches 3; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 3 CXXXXXXCXXXXXXCXXXXXXH 24
 DB 53 CSSISFCSLASSAELRYSSSH 74

RESULT 2

O7PER7 PRELIMINARY; PRT; 39 AA.
 AC O7PER7;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE ENSANGP0000023374.
 GN Name=ENSANG0000020343;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; AA001008326; EAA45619.1; -.
 SQ SEQUENCE 39 AA; 4317 MW; 6963C9D228D7C8C7 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 39;
 Best Local Similarity 28.6%; Pred. No. 6.5e+02;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CXXXXXC 9
 DB 2 CAATASC 8

RESULT 3

O7UWS9 PRELIMINARY; PRT; 49 AA.
 AC O7UWS9;
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RB1825;
 OS Rhodopirella baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,

RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete *Pirellula* sp.
 RT strain 1."; Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 RL EMBL; BX294135; CAD72283.1; --
 DR EMBL; BX294135; CAD72283.1; --
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 49 AA; 5561 MW; D47FD5A9BFF7BA40 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 49;
 Best Local Similarity 28.6%; Pred. No. 7.5e+02; Indels 5; Gaps 0;
 Matches 2; Conservative 0; Mismatches 5;

Qy 3 CXXXXXC 9
 |
 Db 3 CSSASC 9

RESULT 4

Q7PE97 PRELIMINARY; PRT; 58 AA.
 AC Q7PE97;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000022719 (Fragment).
 GN Name=ENSANGP0000022719 (Fragment).
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01004888; EAA45826.1; --
 FT NON_TER 1 58
 FT NON_TER 58
 SQ SEQUENCE 58 AA; 6678 MW; BDD2E5D73967DAB5 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 58;
 Best Local Similarity 28.6%; Pred. No. 8.4e+02; Indels 5; Gaps 0;
 Matches 2; Conservative 0; Mismatches 5;

Qy 3 CXXXXXC 9
 |
 Db 28 CAATASC 34

RESULT 5

Q86YX3 PRELIMINARY; PRT; 61 AA.
 AC Q86YX3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MTE.
 GN Name=MTE;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Qy L.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -! FUNCTION: Metallothioneins have a high content of cysteine
 CC residues that bind various heavy metals (By similarity).
 CC -! SIMILARITY: Belongs to the metallothionein superfamily. Family 1.

DR EMBL; AF348997; AAO32957.1; --
 DR HSP; P02795; 1MHU.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR InterPro; IPR003019; Metallthion_.
 DR InterPro; IPR000006; Metallthion_.
 DR Pfam; PF00131; Metallothio; 1.
 DR PRINTS; PR00860; MTVERTEBRATE.
 KW Metal-binding; Metal-thiolate cluster.
 SQ SEQUENCE 61 AA; 6165 MW; 7F71CE7D1C37762A CRC64;

Query Match 33.3%; Score 18; DB 2; Length 61;
 Best Local Similarity 28.6%; Pred. No. 8.7e+02; Indels 5; Gaps 0;
 Matches 2; Conservative 0; Mismatches 5;

Qy 3 CXXXXXC 9
 |
 Db 7 CSTSSC 13

RESULT 6

CMC1_EIMAC STANDARD; PRT; 79 AA.
 AC P21959;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE EAMZP30-47 protein (Fragment).
 GN Name=CMC17;
 OS Eimeria acervulina.
 OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
 OC Eimeria.
 OX NCBI_TaxID=5801;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9018433; PubMed=1690144; DOI=10.1016/0014-4894(90)90117-U;
 RA Jenkins M.C., Lillehoj H.S., Barta J.R., Danforth H.D.,
 RA Strohllein D.A.;
 RT "Eimeria acervulina: cloning of a cDNA encoding an immunogenic region
 RT of several related merozoite surface and rhoptry proteins."; J.
 RL Exp. Parasitol. 70:353-362(1990).
 CC -! SUBCELLULAR LOCATION: Surface membrane and internal rhoptries.
 CC -! DEVELOPMENTAL STAGE: Merozoite.
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 DR EMBL; M37843; AAA62796.1; --
 KW Antigen; Membrane; Merozoite.
 FT NON_TER 1 79
 FT NON_TER 79
 SQ SEQUENCE 79 AA; 8703 MW; 0B2B6CDB65FB4330 CRC64;

Query Match 33.3%; Score 18; DB 1; Length 79;
 Best Local Similarity 28.6%; Pred. No. 1e+03; Indels 5; Gaps 0;
 Matches 2; Conservative 0; Mismatches 5;

Qy 3 CXXXXXC 9
 |
 Db 30 CSSSSC 36

RESULT 7

Q7PE39 PRELIMINARY; PRT; 87 AA.
 AC Q7PE39;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE ENSANGP0000023751 (Fragment).
 GN Name=ENSANGG0000020038
 OS Anopheles gambiae str. FEST.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; ABA01002921; EAA45886.1; --
 FT NON_TER 1
 FT NON_TER 87
 SQ SEQUENCE 87 AA; 10053 MW; 45F57BD9A1AE0FC3 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 87;
 Best Local Similarity 28.6%; Pred. No. 1.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 Db 28 CAATASC 34
 RESULT 8
 Q94AZ8
 ID Q94AZ8 PRELIMINARY; PRT; 88 AA.
 AC Q94AZ8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE AT4G2230/T10114 60 (Hypothetical protein).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P.,
 RA Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A.,
 RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J.,
 RA Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2008475; PubMed=12093376;
 RA Haas B.J., Volforsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation."
 RN Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY045581; AAK73939.1; --
 DR EMBL; AY084624; AAM61187.1; --
 DR EMBL; AY094030; AAM16186.1; --
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR003614; Koot1.
 DR SMART; SM00505; Koot1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 88 AA; 9071 MW; 2345DAB2B66E96A8 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 88;
 Best Local Similarity 28.6%; Pred. No. 1.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 Db 40 CTSSSTC 46
 RESULT 9
 Q63316
 ID Q63316 PRELIMINARY; PRT; 111 AA.
 AC Q63316
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ly6-A antigen (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=90152758; PubMed=2154400;
 RA Friedman S., Palfree R.G.E., Sirlin S., Haemmerling U.;
 RT "Analysis of three distinct Ly6-A-related cDNA sequences isolated from
 RT rat kidney."
 RL Immunogenetics 31:104-111(1990).
 DR EMBL; M30692; AAA41545.1; --
 DR HSSP; Q9Y111; 1HC9.
 DR InterPro; IPR001526; LY6 UPAR.
 DR Pfam; PF00021; UPAR_LY6_1.
 DR SMART; SM00134; LU; 1.
 FT NON_TER 111
 SQ SEQUENCE 111 AA; 11755 MW; BOA42D1B3ED148C4 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 111;
 Best Local Similarity 28.6%; Pred. No. 1.3e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 Db 17 CSSTATC 23
 RESULT 10
 Q6K499
 ID Q6K499 PRELIMINARY; PRT; 113 AA.
 AC Q6K499;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OJ1595_D08.20.
 GN Name=OJ1595_D08.20;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Magnoliaceae; Oryzae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsunoto T., Hattori M., Sakaki Y., Katayose Y.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005574; BAD22270.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 113 AA; 12326 MW; C2A6C98129828244 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 113;
 Best Local Similarity 28.6%; Pred. No. 1.3e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 35 CSASACA 41
 RESULT 11
 ID O40635 PRELIMINARY; PRT; 116 AA.
 AC O40635;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE CD59 protein (Viral CD59 antigen).
 GN Name=orf15; Synonym=VCD59;
 OS Saimiriine herpesvirus 2.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=10381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-488;
 RX MEDLINE=98037620; PubMed=9371569;
 RA Knappe A., Hiller C., Thura M., Wittmann S., Hofmann H.,
 RA Fleckenstein B., Fickenscher H.;
 RT "The superantigen-homologous viral immediate-early gene iel4/vseg in
 RT herpesvirus saimiri-transformed human T cells.";
 RL J. Virol. 71:9124-9133(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C488;
 RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
 RA Essner A., Thura M., Wittmann S., Fickenscher H.;
 RT "The genome of herpesvirus saimiri C488 which is capable of
 RT transforming human T cells";
 RL Virology 314:471-487(2003).
 DR EMBL; Y13183; CAA73629.1; --
 DR EMBL; AJ410493; CAC94310.1; --
 DR HSSP; P13987; IERG.
 DR InterPro; IPR003632; LY-6_CD59.
 DR Pfam; PF00021; UPAR_LY6_1
 DR ProDom; PD003128; LY-6_CD59; 1.
 DR SMART; SM00134; LU; 1.
 DR PROSITE; PS00983; LY6_UPAR; 1.
 KW Glycoprotein; GPI-anchor; Lipoprotein; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 96 Surface glycoprotein CD59 homolog.
 FT PROPEP 97 121 Removed in mature form (Potential).
 FT DOMAIN 20 104 UPAR/LY6.
 FT DISULFID 22 45 By similarity.
 FT DISULFID 25 32 By similarity.
 FT DISULFID 38 58 By similarity.
 FT DISULFID 64 82 By similarity.
 FT DISULFID 83 88 By similarity.
 FT LIPID 96 96 GPI-anchor amidated asparagine (by host)
 FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 116 AA; 13172 MW; 68E35CE923FF189 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 116;
 Best Local Similarity 28.6%; Pred. No. 1.3e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 32 CTTSTSC 38
 RESULT 12
 ID CD59_SHV21 STANDARD; PRT; 121 AA.
 AC Q00956;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Surface glycoprotein CD59 homolog precursor.
 GN Name=15;
 OS Saimiriine herpesvirus 2 (strain 11) (SAHV-2) (Herpesvirus saimiri).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=10383;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92333688; PubMed=1321287;
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
 RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
 RA Honess R.W.;
 RT "Primary structure of the herpesvirus saimiri genome.";
 RL J. Virol. 66:5047-5058(1992).
 RN [2]
 RP SIMILARITY TO CD59.
 RX MEDLINE=92410640; PubMed=1382344;
 RA Albrecht J.-C., Nicolas J., Newman C., Fleckenstein B.,
 RA Honess R.W.;
 RT "Herpesvirus saimiri has a gene specifying a homologue of the cellular
 RT membrane glycoprotein CD59.";
 RL Virology 190:527-530(1992).
 CC -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -|- SIMILARITY: Contains 1 UPAR/LY6 domain.
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 CC EMBL; X64346; CAA45638.1; --
 DR EMBL; X64273; CAA45565.1; --
 DR HSSP; P13987; IERG.
 DR InterPro; IPR003632; LY-6_CD59.
 DR InterPro; IPR001526; LY6_UPAR.
 DR Pfam; PF00021; UPAR_LY6_1.
 DR ProDom; PD003128; LY-6_CD59; 1.
 DR SMART; SM00134; LU; 1.
 DR PROSITE; PS00983; LY6_UPAR; 1.
 KW Glycoprotein; GPI-anchor; Lipoprotein; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 96 Surface glycoprotein CD59 homolog.
 FT PROPEP 97 121 Removed in mature form (Potential).
 FT DOMAIN 20 104 UPAR/LY6.
 FT DISULFID 22 45 By similarity.
 FT DISULFID 25 32 By similarity.
 FT DISULFID 38 58 By similarity.
 FT DISULFID 64 82 By similarity.
 FT DISULFID 83 88 By similarity.
 FT LIPID 96 96 GPI-anchor amidated asparagine (by host)
 FT CARBOHYD 24 24 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 121 AA; 13814 MW; 56A8BDC07B953AA3 CRC64;
 Query Match 33.3%; Score 18; DB 1; Length 121;
 Best Local Similarity 28.6%; Pred. No. 1.3e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 32 CTTSTSC 38
 RESULT 13
 ID Q9GM28 PRELIMINARY; PRT; 124 AA.
 AC Q9GM28;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain parietal lobe;
 RX MEDLINE=2145851; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
 RA Oeda N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
 RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
 RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
 chromosomes.";
 RL Gene 275:31-37(2001).
 DR EMBL; AB049858; BAB16744.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 124 AA; 13904 MW; B87262632AF6D149 CRC64;

 Query Match 33.3%; Score 18; DB 2; Length 124;
 Best Local Similarity 28.6%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

 QY 3 CXXXXXC 9
 Db 16 CAASSTC 22

 RESULT 14
 Q6ILG2 PRELIMINARY; PRT; 129 AA.
 AC Q6ILG2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE HDC09485.
 GN ORFNames=HDC09485;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;
 RA Hild M., Beckmann B., Haas S., Koch B., Solovjev V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohnsbeil J., Paro R.;
 RT "An integrated gene annotation and transcriptional profiling approach
 RT towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:R3-R3(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 DR EMBL; BK002054; DRA02899.1; -;
 SQ SEQUENCE 129 AA; 13635 MW; 1E5850AE37A3F647 CRC64;

 Query Match 33.3%; Score 18; DB 2; Length 129;
 Best Local Similarity 28.6%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

 QY 3 CXXXXXC 9
 Db 91 CSSTSC 97

 RESULT 15
 Q8N7Z3 PRELIMINARY; PRT; 131 AA.
 AC Q8N7Z3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ40194.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakatsuki A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa B., Omura Y.,
 RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirao K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shionhara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK037513; BAC05083.1; -;
 SQ SEQUENCE 131 AA; 14426 MW; 39A5B4F52922BB2D CRC64;

 Query Match 33.3%; Score 18; DB 2; Length 131;
 Best Local Similarity 28.6%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

 QY 3 CXXXXXC 9
 Db 113 CTATTAC 119

 RESULT 16
 Q63317 PRELIMINARY; PRT; 135 AA.
 ID Q63317;
 AC Q63317;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Rat Ly6-B antigen.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90152758; PubMed=2154400;
 RA Friedman S., Palfrey R.G.E., Sirin S., Haemmerling U.;
 RT "Analysis of three distinct Ly6-A-related cDNA sequences isolated from
 RT rat kidney.";
 RL Immunogenetics 31:104-111(1990).
 DR EMBL; M30689; AAA1546.1; -;
 DR PIR; A45835; A45835.
 DE HSSP; Q9Y111; 2ABX.

DR InterPro; IPR001526; LY6 UPAR.
 DR Pfam; PF00021; UPAR_LY6; 1.
 DR SMART; SM00134; LU; 1.
 SQ SEQUENCE 135 AA; 14130 MW; E4D6ADC56B61A053 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 135;
 Best Local Similarity 28.6%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
 Db 41 CSSTATC 47

RESULT 17
 ID Q24987 PRELIMINARY; PRT; 137 AA.
 AC Q24987;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Surface protein (Fragment).
 GN Name=tpg;
 OS Giardia lamblia (Giardia intestinalis).
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiae; Giardia.
 OX NCBI_TaxID=5741;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA EY P.L., Darby J.M., Mayrhofer G.;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L16973; AAB59198.1; -.
 DR InterPro; IPR005127; Giardia.VSP.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR Pfam; PF03302; VSP; 1.
 FT NON_TER 1
 FT NON_TER 137
 FT NON_TER 137
 SQ SEQUENCE 137 AA; 14148 MW; A340072153005D58 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 137;
 Best Local Similarity 28.6%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
 Db 103 CTTSSAC 109

RESULT 18
 Q8C2X1
 ID Q8C2X1 PRELIMINARY; PRT; 138 AA.
 AC Q8C2X1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330019L22 product:hypothetical protein, full insert sequence.
 DE Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6875(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK087776; BAC39998.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 138 AA; 14564 MW; 42565D90452C4749 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 138;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
 Db 90 CSSSSAC 96

RESULT 19
 Q6LBB8 PRELIMINARY; PRT; 139 AA.
 ID Q6LBB8
 AC Q6LBB8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Oligotropha carboxydovorans (Pseudomonas carboxydovorans).
 OG Plasmid pHC3.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiales; Oligotropha.

OX NCBI_TaxID=40137;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OM5;
 RX MEDLINE=95238294; PubMed=7721710;
 RA Schuebel U., Kraut M., Moersdorf G., Meyer O.;
 RT "Molecular characterization of the gene cluster encoding the
 RT molybdenum-containing carbon monoxide dehydrogenase of *Oligotropha*
 RT carboxidovorans";
 RL J. Bacteriol. 177:2197-2197(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OM5;
 RX MEDLINE=97464431; PubMed=9324252;
 RA Santiago B., Meyer O.;
 RT "Purification and molecular characterization of the H2 uptake
 RT membrane-bound NiFe-hydrogenase from the carboxidotrophic bacterium
 RT *Oligotropha carboxidovorans*";
 RL J. Bacteriol. 179:6053-6060(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OM5;
 RA Santiago B., Schuebel U., Egeleer C., Meyer O.;
 RT "Sequence analysis, characterization and CO-specific transcription of
 RT the cox gene cluster on the megaplasmid pHC3 of *Oligotropha*
 RT carboxidovorans";
 RL Gene 236:1157-1247(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OM5;
 RX PubMed=14644498; DOI=10.1016/j.gene.2003.08.027;
 RA Fuhrmann S., Ferner M., Jeffke T., Henne A., Gottschalk G., Meyer O.;
 RT "Complete nucleotide sequence of the self-transmissible circular
 RT megaplasmid pHC3 of *Oligotropha carboxidovorans*: Function in the
 RT chemolithoautotrophic utilization of CO, H2 and CO2";
 RL Gene 322:67-75(2003).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OM5;
 RA Schuebel U.;
 RT Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OM5;
 RA Fuhrmann S.;
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; X82447; CAG28441.1; -;
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 139 AA; 15501 MW; F67DC09839ABFA6A CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 139;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXX 9
 DB 103 CASSTSC 109
 RESULT 20
 Q96AC2
 ID Q96AC2 PRELIMINARY; PRT; 141 AA.
 AC Q96AC2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein FLJ37182 (PSCA Hlog).
 GN ORFName=UNQ3079;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.W., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Alzheimer cortex;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakatsuki A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori K.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Mutsaers H., Yuuki H., Ooshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Okamoto S.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Senba T.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yanashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isigaki T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vasta A.,
 RA Vandlen R., Watanabe C., Wieand D., Woodde K., Xie M.H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; BC017318; RAH17318.1; -;
 DR EMBL; AK094501; BAC04368.1; -;
 DR EMBL; AY358628; AAQ89991.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 141 AA; 15240 MW; CFA6D98BA90792E3 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 141;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 3 CXXXXXX 9
 DB 71 CASSAAC 77
 RESULT 21
 ID Q66H42 PRELIMINARY; PRT; 141 AA.
 AC Q66H42;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
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 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Director MGC Project;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC082032; AAH82032.1; -;
 DR InterPro; IPR001526; LY6 UPAR.
 DR Pfam; PF00021; UPAR_LY6; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 141 AA; 15330 MW; BB8CC9993E322DA2 CRC64;
 Query Match 33.3%; Score 18; DB 2; Length 141;
 Best Local Similarity 28.6%; Pred. No. 1.5e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 3 CXXXXXX 9

DB 71 CASSAAC 77
 RESULT 22
 ID Q8BLC3 PRELIMINARY; PRT; 141 AA.
 AC Q8BLC3;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
 DE enriched library, clone:B230214B19 product:hypothetical Snake toxin-
 DE like structure containing protein, full insert sequence (Similar to
 DE human MGC39643 protein).
 GN Name=2700050C12Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
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 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
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 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
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 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
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 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
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 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
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 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipillar sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Izawa M., Izawa K., Tanaka T., Matsura S., Kawai J.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipillar sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Izawa M., Izawa K., Tanaka T., Matsura S., Kawai J.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipillar sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Izawa M., Izawa K., Tanaka T., Matsura S., Kawai J.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipillar sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Izawa M., Izawa K., Tanaka T., Matsura S., Kawai J.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multipillar sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayaishizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[7]
RN
RP
SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[8]
RN
RP
SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK045592; BAC32428.1; -;
DR EMBL; BC058599; AAH58599.1; -;
DR MGD; MGI:1919835; 2700050C12Rik.
DR GO; GO:0016526; F:G-protein coupled receptor activity, unknown. . .; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
KW Hypothetical protein.
SQ SEQUENCE 141 AA; 15261 MW; 51717F7922C02DAA CRC64;
Query Match 33.3%; Score 18; DB 2; Length 141;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 CXXXXXC 9
Db 71 CASSAAC 77
RESULT 23
Q9JJ96 PRELIMINARY; PRT; 141 AA.
AC Q9JJ96
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus brain cDNA, clone MNCB-0671.
GN Name=2700050C12Rik;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041649; BAA95101.1; -;

DR MGD; MGI:1919835; 2700050C12Rik.
DR GO; GO:0016526; F:G-protein coupled receptor activity, unknown. . .; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR001526; LV6_UPAR.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 141 AA; 15231 MW; C8716DDC652288ED CRC64;
Query Match 33.3%; Score 18; DB 2; Length 141;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 CXXXXXC 9
Db 71 CASSAAC 77
RESULT 24
UL42 HCMVA
ID UL42 HCMVA STANDARD; PRT; 157 AA.
AC P16815;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein UL42.
GN Name=UL42;
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchison C.A. III, Kourazides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
cytomegalovirus strain AD169";
RL Curr. Top. Microbiol. Immunol. 154:125-169 (1990).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; X17403; CAA35401.1; -;
DR PIR; S09805; S09805.
KW Hypothetical protein.
FT CARBOHYD 147 147
SQ SEQUENCE 157 AA; 17066 MW; 59BFBI5443124954 CRC64;
N-linked (GlcNAc. . .) (Potential).
Query Match 33.3%; Score 18; DB 1; Length 157;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3 CXXXXXC 9
Db 76 CAATSSC 82
RESULT 25
Q6ZP52 PRELIMINARY; PRT; 157 AA.
AC Q6ZP52
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ26495.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130005; BAC85273.1; -;
SQ SEQUENCE 157 AA; 16919 MW; 126998C032DB6AC5 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 157;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 87 CASSAAC 93

RESULT 26
Q7QF28 PRELIMINARY; PRT; 160 AA.
AC Q7QF28;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP13679 (Fragment).
GN Name=agCG54781; ORFNames=ENSANGG00000010518;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008846; EAA06475.1; -;
DR InterPro; IPR008597; Destabilase.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF05497; Destabilase; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 160 AA; 17368 MW; BEFA5PB917ACC080 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 160;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 45 CSTSTTC 51

RESULT 27
Q88EY6 PRELIMINARY; PRT; 162 AA.
AC Q88EY6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PP4314;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016790; AAN69894.1; -;
DR TIGR; PA3114; -;
DR GO; GO:0016846; P:carbon-sulfur lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR006913; GFA.
DR Pfam; PF04828; DUF636; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 162 AA; 18077 MW; 6PFS14D988E63BD3 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 162;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 2 CTSSTAC 8

RESULT 28
Q6ZW14 PRELIMINARY; PRT; 164 AA.
AC Q6ZW14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ41033.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Chiba Y.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK123029; BAC85518.1; -;
SQ SEQUENCE 164 AA; 17762 MW; EF4A4BCB69DA1252 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 164;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 94 CASSAAC 100

RESULT 29
Q8N2G4 PRELIMINARY; PRT; 165 AA.
ID Q8N2G4
AC Q8N2G4;

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Wed Apr 27 17:41:54 2005

DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein PSEC0181.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagehara K., Sugano S., Isogai T.,
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075487; BAC11647.1; -.
DR InterPro; IPR001526; LY6_UPAR.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 165 AA; 17900 MW; 2B0B8D68044C8999 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 165;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
Db 71 CASSAAC 77

RESULT 30
Q24969 PRELIMINARY; PRT; 167 AA.
AC Q24969;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Giardia lamblia WB putative surface antigen (Fragment).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=WB;
RA Hilario E., Gogarten J.,
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10907; AAA19317.1; -.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR009030; Grow fac recept.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
FT NON_TER 1_1
SQ SEQUENCE 167 AA; 17671 MW; FDAB0A43EC276EDC CRC64;

Query Match 33.3%; Score 18; DB 2; Length 167;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
Db 71 CSSAASC 77

Search completed: April 27, 2005, 16:41:38
Job time : 177 secs

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2	18	33.3	15	4	US-09-142-524D-142
3	18	33.3	24	4	US-09-731-243A-3
4	18	33.3	34	4	US-09-270-767-40588
5	18	33.3	34	4	US-09-270-767-55804
6	18	33.3	36	4	US-09-816-721-1
7	18	33.3	48	5	PT-US96-01720-8
8	18	33.3	50	3	US-08-900-230-58
9	18	33.3	70	4	US-09-621-976-6084
10	18	33.3	90	4	US-09-419-381-90
11	18	33.3	125	4	US-09-252-991A-27726
12	18	33.3	127	3	US-08-467-023-189
13	18	33.3	132	4	US-09-252-991A-22556
14	18	33.3	134	4	US-09-252-991A-25069
15	18	33.3	138	4	US-09-252-991A-16583
16	18	33.3	139	4	US-09-252-991A-29513
17	18	33.3	141	4	US-09-825-294-215
18	18	33.3	141	4	US-09-970-966-215
19	18	33.3	143	4	US-09-252-991A-17322
20	18	33.3	148	4	US-09-252-991A-17476
21	18	33.3	148	4	US-09-252-991A-23009
22	18	33.3	152	4	US-09-252-991A-24277
23	18	33.3	156	4	US-09-252-991A-31875
24	18	33.3	158	4	US-09-252-991A-30633
25	18	33.3	163	2	US-08-727-688-25
26	18	33.3	163	4	US-09-252-991A-29098
27	18	33.3	166	4	US-09-252-991A-27896
					Sequence 141, Appl
					Sequence 142, App
					Sequence 3, Appl
					Sequence 40588, A
					Sequence 55804, A
					Sequence 1, Appli
					Sequence 8, Appli
					Sequence 58, Appl
					Sequence 6084, Ap
					Sequence 90, Appl
					Sequence 27726, A
					Sequence 189, App
					Sequence 22556, A
					Sequence 25069, A
					Sequence 16583, A
					Sequence 29513, A
					Sequence 215, App
					Sequence 215, App
					Sequence 17322, A
					Sequence 17476, A
					Sequence 23009, A
					Sequence 24277, A
					Sequence 31875, A
					Sequence 30633, A
					Sequence 25, Appl
					Sequence 29098, A
					Sequence 27896, A

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102 17 31.5 18 2 US-08-169-948B-48
103 17 31.5 18 2 US-08-448-873-48
104 17 31.5 20 2 US-08-637-759B-145
105 17 31.5 20 3 US-08-871-355A-145
106 17 31.5 20 3 US-08-476-509B-47
107 17 31.5 20 3 US-08-467-023-54
108 17 31.5 20 3 US-09-201-945-145
109 17 31.5 20 4 US-09-148-545-227
110 17 31.5 24 4 US-08-900-230-34
111 17 31.5 24 4 US-09-643-657-41
112 17 31.5 25 2 US-08-754-431A-11
113 17 31.5 25 3 US-08-900-230-38
114 17 31.5 29 3 US-09-136-769A-5
115 17 31.5 29 3 US-09-136-769A-16
116 17 31.5 31 2 US-08-169-948B-2
117 17 31.5 31 2 US-08-448-873-2
118 17 31.5 31 2 US-08-382-452D-2
119 17 31.5 31 4 US-09-916-494A-2
120 17 31.5 32 1 US-07-952-735A-3
121 17 31.5 32 1 US-07-952-735A-4
122 17 31.5 32 2 US-08-595-868C-41
123 17 31.5 32 3 US-09-139-819A-41
124 17 31.5 32 4 US-09-750-913-41
125 17 31.5 32 6 5183802-5
126 17 31.5 32 6 5183802-5
127 17 31.5 33 1 US-07-776-272-9
128 17 31.5 33 2 US-08-169-948B-6
129 17 31.5 33 2 US-08-448-873-6
130 17 31.5 33 3 US-08-382-452D-6
131 17 31.5 33 4 US-08-507-362A-2
132 17 31.5 33 4 US-09-916-494A-6
133 17 31.5 34 1 US-07-952-735A-1
134 17 31.5 34 1 US-07-952-735A-2
135 17 31.5 36 4 US-09-166-966E-5
136 17 31.5 38 3 US-08-900-230-55
137 17 31.5 39 2 US-08-169-948B-4
138 17 31.5 39 2 US-08-448-873-4
139 17 31.5 39 3 US-08-382-452D-4
140 17 31.5 39 4 US-09-916-494A-4
141 17 31.5 44 1 US-08-676-169-6
142 17 31.5 44 3 US-09-063-431A-6
143 17 31.5 44 4 US-09-166-966E-9
144 17 31.5 45 1 US-08-451-947-97
145 17 31.5 45 1 US-08-451-947-98
146 17 31.5 45 1 US-08-451-947-99
147 17 31.5 45 1 US-08-451-947-100
148 17 31.5 45 2 US-08-424-826A-11
149 17 31.5 45 2 US-08-424-826A-12
150 17 31.5 45 2 US-08-424-826A-97

ALIGNMENTS

RESULT 1
US-09-142-524D-141
; Sequence 141, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 141
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 58
US-09-142-524D-141

Query Match 33.3%; Score 18; DB 4; Length 15;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 8 CTSASAC 14

RESULT 2

US-09-142-524D-142
; Sequence 142, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:

; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; CURRENT FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 59
US-09-142-524D-142

Query Match 33.3%; Score 18; DB 4; Length 15;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 3 CTSASAC 9

RESULT 3

US-09-731-242A-3
; Sequence 3, Application US/09731242A
; Patent No. 6759243
; GENERAL INFORMATION:

; APPLICANT: Kranz, David
; APPLICANT: Wittrup, K. Dane
; APPLICANT: Holler, Phillip
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 24

; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1..1)

; OTHER INFORMATION: upstream primer

US-09-731-242A-3

Query Match 33.3%; Score 18; DB 4; Length 24;

Best Local Similarity 28.6%; Pred. No. 2.4e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 CXXXXXC 9

Db 9 CATAAAC 15

RESULT 4

US-09-270-767-40588

; Sequence 40588, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 40588

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-40588

Query Match 33.3%; Score 18; DB 4; Length 34;

Best Local Similarity 28.6%; Pred. No. 2.4e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 CXXXXXC 9

Db 4 CSSSSC 10

RESULT 5

US-09-270-767-55804

; Sequence 55804, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 55804

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-55804

Query Match 33.3%; Score 18; DB 4; Length 34;

Best Local Similarity 28.6%; Pred. No. 2.4e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 CXXXXXC 9

Db 4 CSSSSC 10

RESULT 6

US-09-816-721-1

; Sequence 1, Application US/09816721

; Patent No. 6777215

; GENERAL INFORMATION:

; APPLICANT: No. 6777215ozymes A/S

; APPLICANT: Andersen, Carsten

; APPLICANT: Nielsen, Bjarne R.

; APPLICANT: Haren, Lubbet D.

; APPLICANT: Dijkstra, Bauke H.

; TITLE OF INVENTION: No. 6777215el Cyclomaltodextrin Glucanotransferase Variants

; FILE REFERENCE: 5347.210-US

; CURRENT APPLICATION NUMBER: US/09/816,721

; CURRENT FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic

; NAME/KEY: misc_feature

; OTHER INFORMATION: "DI96H oligo"

US-09-816-721-1

Query Match 33.3%; Score 18; DB 4; Length 36;

Best Local Similarity 28.6%; Pred. No. 2.5e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 CXXXXXC 9

Db 25 CTAAATC 31

RESULT 7

PCT-US96-01720-8

; Sequence 8, Application PC/TUS9601720

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN

; NUMBER OF SEQUENCES: 11

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/01720

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/387,055

; FILING DATE: 09-FEB-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCE/DOCKET NUMBER: 16336-SPC

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 48 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US96-01720-8

Query Match 33.3%; Score 18; DB 5; Length 48;

Best Local Similarity 28.6%; Pred. No. 2.9e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 CXXXXXC 9

✓

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27726

Query Match 33.3%; Score 18; DB 4; Length 125;
Best Local Similarity 28.6%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 17 CTAATTC 23

RESULT 12

US-08-467-023-189
Sequence 189, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESS: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 189:

SEQUENCE CHARACTERISTICS:

LENGTH: 127 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-467-023-189

Query Match 33.3%; Score 18; DB 3; Length 127;
Best Local Similarity 28.6%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 77 CTSASAC 83

RESULT 13

US-09-252-991A-22556
Sequence 22556, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22556

LENGTH: 132

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22556

Query Match 33.3%; Score 18; DB 4; Length 132;

Best Local Similarity 28.6%; Pred. No. 4.9e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 33 CSAASAC 39

RESULT 14

US-09-252-991A-25069
Sequence 25069, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25069

LENGTH: 134

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25069

Query Match 33.3%; Score 18; DB 4; Length 134;

Best Local Similarity 28.6%; Pred. No. 4.9e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 11 CSAATTC 17

RESULT 15

US-09-252-991A-16583
Sequence 16583, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16583
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16583

Query Match 33.3%; Score 18; DB 4; Length 138;
Best Local Similarity 28.6%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 53 CASTTAC 59

RESULT 16

US-09-252-991A-29513
; Sequence 29513, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29513
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29513

Query Match 33.3%; Score 18; DB 4; Length 139;
Best Local Similarity 28.6%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 48 CSTSTAC 54

RESULT 17

US-09-825-294-215
; Sequence 215, Application US/09825294
; Patent No. 6710170
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolck, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 215
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-294-215

Query Match 33.3%; Score 18; DB 4; Length 143;
Best Local Similarity 28.6%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 114 CASSTAC 120

RESULT 20

US-09-252-991A-17476

Query Match 33.3%; Score 18; DB 4; Length 141;
Best Local Similarity 28.6%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 71 CASSAAC 77

RESULT 18

US-09-970-966-215
; Sequence 215, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolck, John A.
; APPLICANT: Moesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-966-215

Query Match 33.3%; Score 18; DB 4; Length 141;
Best Local Similarity 28.6%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 71 CASSAAC 77

RESULT 19

US-09-252-991A-17322
; Sequence 17322, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17322
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17322

Query Match 33.3%; Score 18; DB 4; Length 143;
Best Local Similarity 28.6%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 114 CASSTAC 120

; Sequence 17476, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 17476

; LENGTH: 148

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17476

Query Match 33.3%; Score 18; DB 4; Length 148;

Best Local Similarity 28.6%; Pred. No. 5.2e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9

Db 18 CTTSSC 24

RESULT 21

US-09-252-991A-23009

; Sequence 23009, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 23009

; LENGTH: 148

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23009

Query Match 33.3%; Score 18; DB 4; Length 148;

Best Local Similarity 28.6%; Pred. No. 5.2e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9

Db 68 CSSSAC 74

RESULT 22

US-09-252-991A-24277

; Sequence 24277, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 24277

; LENGTH: 152

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24277

Query Match 33.3%; Score 18; DB 4; Length 152;

Best Local Similarity 28.6%; Pred. No. 5.3e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9

Db 81 CATSSTC 87

RESULT 23

US-09-252-991A-31875

; Sequence 31875, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 31875

; LENGTH: 156

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31875

Query Match 33.3%; Score 18; DB 4; Length 156;

Best Local Similarity 28.6%; Pred. No. 5.3e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9

Db 26 CSTTASC 32

RESULT 24

US-09-252-991A-30633

; Sequence 30633, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 30633

; LENGTH: 158

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-30633

Query Match 33.3%; Score 18; DB 4; Length 158;

Best Local Similarity 28.6%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 2 CSSATTC 8

RESULT 25

US-08-727-688-25
; Sequence 25, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5919638e
US-08-727-688-25

Query Match 33.3%; Score 18; DB 2; Length 163;
Best Local Similarity 28.6%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 72 CSSSSC 78

RESULT 26

US-09-252-991A-29098
; Sequence 29098, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29098
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29098

Query Match 33.3%; Score 18; DB 4; Length 163;
Best Local Similarity 28.6%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 67 CSSATAC 73

RESULT 27

US-09-252-991A-27896
; Sequence 27896, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27896
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27896

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Best Local Similarity 28.6%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 29 CATSTAC 35

RESULT 28

US-09-252-991A-25719
; Sequence 25719, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25719
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25719

Query Match 33.3%; Score 18; DB 4; Length 174;
Best Local Similarity 28.6%; Pred. No. 5.6e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
|
Db 24 CTASSAC 30

RESULT 29

US-09-252-991A-31386
; Sequence 31386, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31386
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31386

Query Match 33.3%; Score 18; DB 4; Length 178;
Best Local Similarity 28.6%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
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Db 29 CATASTC 35

RESULT 30

US-09-252-991A-17994
; Sequence 17994, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17994
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17994

Query Match 33.3%; Score 18; DB 4; Length 190;
Best Local Similarity 28.6%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
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Db 114 CASTTAC 120

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OM protein - protein search, using sw model

Run on: April 27, 2005, 16:38:46 ; Search time 133 Seconds
(without alignments)
77.568 Million cell updates/sec

Title: US-09-732-348b-34

Perfect score: 54

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Total number of hits satisfying chosen parameters: 1424015

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Maximum Match 100%

Listing first 150 summaries

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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	18	33.3	10	10	US-09-572-404B-2399
5	18	33.3	10	10	US-09-572-404B-2401
6	18	33.3	10	10	US-09-572-404B-2425
7	18	33.3	10	10	US-09-572-404B-2485
8	18	33.3	10	10	US-09-572-404B-2527
9	18	33.3	10	10	US-09-572-404B-2533
10	18	33.3	10	10	US-09-572-404B-2543
11	18	33.3	10	10	US-09-572-404B-2557
12	18	33.3	12	16	US-10-763-992-32
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16	18	33.3	24	9	US-09-731-242A-3	Sequence 3, Appl
17	18	33.3	25	15	US-10-361-811-292	Sequence 292, App
18	18	33.3	25	15	US-10-369-186-292	Sequence 292, App
19	18	33.3	28	9	US-09-864-761-41104	Sequence 41104, A
20	18	33.3	33	16	US-10-697-399-10	Sequence 10, Appl
21	18	33.3	36	9	US-09-816-721-1	Sequence 1, Appl
22	18	33.3	39	14	US-10-029-386-31509	Sequence 31509, A
23	18	33.3	50	8	US-08-900-230-58	Sequence 58, Appl
24	18	33.3	58	14	US-10-039-386-28972	Sequence 28972, A
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32	18	33.3	71	14	US-10-269-806-77	Sequence 77, Appl
33	18	33.3	71	14	US-10-269-806-85	Sequence 85, Appl
34	18	33.3	71	14	US-10-269-806-109	Sequence 109, App
35	18	33.3	71	14	US-10-269-806-117	Sequence 117, App
36	18	33.3	71	14	US-10-269-806-133	Sequence 133, App
37	18	33.3	75	9	US-09-758-140-11	Sequence 11, Appl
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39	18	33.3	81	15	US-10-131-487A-107	Sequence 107, App
40	18	33.3	85	15	US-10-424-599-150900	Sequence 150900, A
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45	18	33.3	91	16	US-10-767-701-56213	Sequence 56213, A
46	18	33.3	104	11	US-09-864-408A-934	Sequence 934, App
47	18	33.3	104	15	US-10-424-599-205166	Sequence 205166, A
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49	18	33.3	106	16	US-10-767-701-51683	Sequence 51683, A
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51	18	33.3	115	15	US-10-369-186-290	Sequence 290, App
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57	18	33.3	123	16	US-10-437-963-161257	Sequence 161257, A
58	18	33.3	131	15	US-10-108-260A-4406	Sequence 4406, App
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61	18	33.3	137	15	US-10-361-811-284	Sequence 284, App
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ALIGNMENTS

RESULT 1
US-09-820-843A-77
; Sequence 77, Application US/09820843A
; Publication No. US200303963A1

; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 77
; LENGTH: 103
; TYPE: PRT
; ORGANISM: M. pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Bol_orf103b Protein
; NAME/KEY: misc feature
; OTHER INFORMATION: gi|1673772
US-09-820-843A-77

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Matches 3; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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US-09-572-404B-2385
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; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2385
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CBA at 82-91 and may interact with Sequence 2
US-09-572-404B-2385

Query Match 33.3%; Score 18; DB 10; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 3 CSSSTTC 9

RESULT 3

US-09-572-404B-2387
; Sequence 2387, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2387
; LENGTH: 10


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; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2527
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C8A at 83-92 and may interact with Sequence 2
; OTHER INFORMATION: this patent.
US-09-572-404B-2527

Query Match      33.3%; Score 18; DB 10; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      2 CSSSTTC 8

RESULT 9
US-09-572-404B-2533
; Sequence 2533, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2533
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C8A at 83-92 and may interact with Sequence 2
; OTHER INFORMATION: this patent.
US-09-572-404B-2533

Query Match      33.3%; Score 18; DB 10; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      2 CSSSTTC 8

RESULT 10
US-09-572-404B-2543
; Sequence 2543, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2543
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C8A at 81-90 and may interact with Sequence 2
; OTHER INFORMATION: this patent.
US-09-572-404B-2543

Query Match      33.3%; Score 18; DB 10; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      2 CSSSTTC 8
```

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Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      4 CSSSTTC 10

RESULT 11
US-09-572-404B-2557
; Sequence 2557, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2557
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C8A at 83-92 and may interact with Sequence 2
; OTHER INFORMATION: this patent.
US-09-572-404B-2557

Query Match      33.3%; Score 18; DB 10; Length 10;
Best Local Similarity 28.6%; Pred. No. 2.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      2 CSSSTTC 8

RESULT 12
US-10-763-992-32
; Sequence 32, Application US/10763992
; Publication No. US20040121397A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; FRIEDMAN, Paula N.
; GORDON, Julian
; HODGES, Steven C.
; KLASS, Michael R.
; KRATOCHVIL, Jon D.
; ROBERTS-RAPP, Lisa
; RUSSELL, John C.
; STROUPE, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/763,992
; FILING DATE: 22-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/418,887
; FILING DATE: 15-OCT-1999
```

APPLICATION NUMBER: US/08/946,869
FILING DATE: 08-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5697.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-763-992-32

Query Match 33.3%; Score 18; DB 16; Length 12;
Best Local Similarity 28.6%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 1 CSSSSC 7

RESULT 13
US-10-354-240-141
Sequence 141, Application US/10354240
Publication No. US20030185847A1
GENERAL INFORMATION:

APPLICANT: Sone, Toshio
APPLICANT: Kume, Akinori
APPLICANT: Dairiki, Kazuo
APPLICANT: Iwama, Akiko
APPLICANT: Kino, Kohsuke
TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
FILE REFERENCE: SPO-103D1
CURRENT APPLICATION NUMBER: US/10/354,240
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: PCT/JP97/00740
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: US 09/142,524
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn version 3.1
SEQ ID NO 141
LENGTH: 15
TYPE: PRT
ORGANISM: Cryptomeria japonica
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(15)
OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 58
US-10-354-240-141

Query Match 33.3%; Score 18; DB 14; Length 15;
Best Local Similarity 28.6%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 8 CTSASAC 14

RESULT 14
US-10-354-240-142
Sequence 142, Application US/10354240
Publication No. US20030185847A1
GENERAL INFORMATION:

APPLICANT: Sone, Toshio
APPLICANT: Kume, Akinori
APPLICANT: Dairiki, Kazuo
APPLICANT: Iwama, Akiko
APPLICANT: Kino, Kohsuke
TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
FILE REFERENCE: SPO-103D1
CURRENT APPLICATION NUMBER: US/10/354,240
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: PCT/JP97/00740
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: US 09/142,524
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn version 3.1
SEQ ID NO 142
LENGTH: 15
TYPE: PRT
ORGANISM: Cryptomeria japonica
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(15)
OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 59
US-10-354-240-142

Query Match 33.3%; Score 18; DB 14; Length 15;
Best Local Similarity 28.6%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 3 CTSASAC 9

RESULT 15
US-10-225-567A-1778
Sequence 1778, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1778
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1778

Query Match 33.3%; Score 18; DB 14; Length 18;
Best Local Similarity 28.6%; Pred. No. 3.3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 9 CASSSC 15

RESULT 16
US-09-731-242A-3
Sequence 3, Application US/09731242A
Patent No. US20020058253A1
GENERAL INFORMATION:
APPLICANT: KRANZ, DAVID
APPLICANT: WITTRUP, K. DANE

; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()
; OTHER INFORMATION: upstream primer
US-09-731-242A-3

Query Match 33.3%; Score 18; DB 9; Length 24;
Best Local Similarity 28.6%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
Db 9 CATAAAC 15

RESULT 17
US-10-361-811-292
; Sequence 292, Application US/10361811
; Publication No. US20030206918A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C8
; CURRENT APPLICATION NUMBER: US/10/361,811
; CURRENT FILING DATE: 2003-02-05
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide used for generation of rabbit
; OTHER INFORMATION: polyclonal anti-sera against O591a.
US-10-361-811-292

Query Match 33.3%; Score 18; DB 15; Length 25;
Best Local Similarity 28.6%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
Db 18 CASSAAC 24

RESULT 18
US-10-369-186-292
; Sequence 292, Application US/10369186
; Publication No. US20030232056A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C9
; CURRENT APPLICATION NUMBER: US/10/369,186

; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 293
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide used for generation of rabbit
; OTHER INFORMATION: polyclonal anti-sera against O591a.
US-10-369-186-292

Query Match 33.3%; Score 18; DB 15; Length 25;
Best Local Similarity 28.6%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
Db 18 CASSAAC 24

RESULT 19
US-09-864-761-41104
; Sequence 41104, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 41104

LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

OTHER INFORMATION: MAP TO AC022045.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
US-09-864-761-41104

Query Match 33.3%; Score 18; DB 9; Length 28;
Best Local Similarity 28.6%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 3 CASSSAC 9

RESULT 20

US-10-697-399-10
Sequence 10, Application US/10697399
Publication No. US20040162413A1

GENERAL INFORMATION:

APPLICANT: Watkins, Jeffrey D.

APPLICANT: Huse, William D.

APPLICANT: Vasserot, Alain P.

APPLICANT: Marquis, David P.

APPLICANT: Smith, Eric P.

TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity

FILE REFERENCE: AME-08122

CURRENT APPLICATION NUMBER: US/10/697,399

CURRENT FILING DATE: 2003-10-30

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PatentIn version 3.2

SEQ ID NO 10

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-697-399-10

Query Match 33.3%; Score 18; DB 16; Length 33;
Best Local Similarity 28.6%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 15 CATTAAC 21

RESULT 21

US-09-816-721-1

Sequence 1, Application US/09816721

Patent No. US20020042120A1

GENERAL INFORMATION:

APPLICANT: No. US20020042120A1ozymes A/S

APPLICANT: Andersen, Carsten

APPLICANT: Nielsen, Bjarne R.

APPLICANT: Haren, Lubbet D.

APPLICANT: Dijkstra, Bauke H.

TITLE OF INVENTION: No. US20020042120A1el Cyclomaltodextrin Glucanotransferase Variants

FILE REFERENCE: 5347.210-US

CURRENT APPLICATION NUMBER: US/09/816,721

CURRENT FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic

NAME/KEY: misc feature

OTHER INFORMATION: "D196H oligo"

US-09-816-721-1

Query Match

33.3%; Score 18; DB 9; Length 36;

Best Local Similarity 28.6%; Pred. No. 4.6e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 25 CTAAATC 31

RESULT 22

US-10-029-386-31509

Sequence 31509, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 31509

LENGTH: 39

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC008456.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.87

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.62

US-10-029-386-31509

Query Match 33.3%; Score 18; DB 14; Length 39;
Best Local Similarity 28.6%; Pred. No. 4.8e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 19 CSATSTC 25

RESULT 23

US-08-900-230-58

Sequence 58, Application US/08900230

Publication No. US20010009766A1

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan A.

TITLE OF INVENTION: DNA ENCODING GALANN GALR3 RECEPTORS AND

TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of The Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 11036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,230
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-900-230-58

Query Match 33.3%; Score 18; DB 8; Length 50;
Best Local Similarity 28.6%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 9 CTAATAC 15

RESULT 24
US-10-029-386-28972
; Sequence 28972, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28972
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.61
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.92
US-10-029-386-28972

Query Match 33.3%; Score 18; DB 14; Length 58;
Best Local Similarity 28.6%; Pred. No. 5.9e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 17 CSSSSAC 23

RESULT 25

US-10-437-963-193586
; Sequence 193586, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 193586
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_89711C.1.pap
US-10-437-963-193586

Query Match 33.3%; Score 18; DB 16; Length 66;
Best Local Similarity 28.6%; Pred. No. 6.3e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 35 CSSASSC 41

RESULT 26
US-10-424-599-202235
; Sequence 202235, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 202235
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_24643C.1.pap
US-10-424-599-202235

Query Match 33.3%; Score 18; DB 15; Length 67;
Best Local Similarity 28.6%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 12 CTTASSC 18

RESULT 27
US-10-424-599-261219
; Sequence 261219, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 261219
LENGTH: 70
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_77903C.1.pap
US-10-424-599-261219

Query Match 33.3%; Score 18; DB 15; Length 70;
Best Local Similarity 28.6%; Pred. No. 6.5e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 5;

QY 3 CXXXXXC 9
DB 23 CSSASSC 29

RESULT 28
US-10-011-931-32
Sequence 32, Application US/10011931
Publication No. US20030026806A1
GENERAL INFORMATION:
APPLICANT: WITTE, ALISON
APPLICANT: VARNUM, BRIAN C.
APPLICANT: QIAN, ZUEMING
APPLICANT: VEZINA, CHRIS
TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BIN
TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF
FILE REFERENCE: A-731
CURRENT APPLICATION NUMBER: US/10/011,931
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: US 60/244,118
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 71
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KAPPA CHAIN CHIMERA
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: At position 1, P = 5' phosphorylated
US-10-011-931-32

Query Match 33.3%; Score 18; DB 14; Length 71;
Best Local Similarity 28.6%; Pred. No. 6.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 5;

QY 3 CXXXXXC 9
DB 45 CTATTAC 51

RESULT 29
US-10-269-806-45
Sequence 45, Application US/10269806
Publication No. US20030176352A1
GENERAL INFORMATION:
APPLICANT: Min, Hosung
APPLICANT: Sitney, Karen
APPLICANT: Hartley, Cynthia

TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic Activity
FILE REFERENCE: A-750
CURRENT APPLICATION NUMBER: US/10/269,806
CURRENT FILING DATE: 2002-10-10
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 71
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized Peptide Sequence
US-10-269-806-45

Query Match 33.3%; Score 18; DB 14; Length 71;
Best Local Similarity 28.6%; Pred. No. 6.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 5;

QY 3 CXXXXXC 9
DB 32 CTAAAC 38

RESULT 30
US-10-269-806-61
Sequence 61, Application US/10269806
Publication No. US20030176352A1
GENERAL INFORMATION:
APPLICANT: Min, Hosung
APPLICANT: Sitney, Karen
APPLICANT: Hartley, Cynthia
TITLE OF INVENTION: Peptides and Related Compounds Having Thrombopoietic Activity
FILE REFERENCE: A-750
CURRENT APPLICATION NUMBER: US/10/269,806
CURRENT FILING DATE: 2002-10-10
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 71
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized Peptide Sequence
US-10-269-806-61

Query Match 33.3%; Score 18; DB 14; Length 71;
Best Local Similarity 28.6%; Pred. No. 6.6e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 5;

QY 3 CXXXXXC 9
DB 44 CTTTTTC 50

Search completed: April 27, 2005, 16:48:17
Job time : 136 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	19	35.2	103	7	ABO23576	AbO23576 Mycoplasma	
2	18	33.3	10	2	Aaw65945	Aaw65945 Molecule	
3	18	33.3	10	4	AAG96291	AAG96291 Human com	
4	18	33.3	10	4	AAG96207	AAG96207 Human com	
5	18	33.3	10	4	AAG96231	AAG96231 Human com	
6	18	33.3	10	4	AAG96205	AAG96205 Human com	
7	18	33.3	10	4	AAG96349	AAG96349 Human com	
8	18	33.3	10	4	AAG96191	AAG96191 Human com	
9	18	33.3	10	4	AAG96339	AAG96339 Human com	
10	18	33.3	10	4	AAG96363	AAG96363 Human com	
11	18	33.3	10	4	AAG96333	AAG96333 Human com	
12	18	33.3	10	4	AAG96193	AAG96193 Human com	
13	18	33.3	12	2	Aaw54432	Aaw54432 Human P51	
14	18	33.3	12	8	ABO8422	ABO8422 Antigen p	
15	18	33.3	12	8	ADQ96644	ADQ96644 Human P51	
16	18	33.3	15	2	AAR97928	Aar-97928 Japan ced	
17	18	33.3	15	2	AAR97929	Aar-97929 Japan ced	
18	18	33.3	18	6	ABP83105	ABP83105 G protein	
19	18	33.3	20	2	Aaw42192	Aaw42192 T-cell ep	
20	18	33.3	25	7	ADM10961	ADM10961 Human ova	
21	18	33.3	25	8	ADJ11291	ADJ11291 Rabbit an	
22	18	33.3	28	4	ABB42303	ABb42303 Peptide #	
23	18	33.3	28	4	AAM36111	Aam36111 Peptide #	
24	18	33.3	28	4	ABE25806	ABE25806 Protein #	
25	18	33.3	28	4	AAM76003	Aam76003 Human bon	

99 18 33.3 141 7 ADC48965 Adc48965 Novel hum
 100 18 33.3 141 7 ADC49482 Adc49482 Novel hum
 101 18 33.3 141 7 ADC47343 Adc47343 Novel hum
 102 18 33.3 141 7 ADC47088 Adc47088 Novel hum
 103 18 33.3 141 7 ADC77963 Adc77963 Novel hum
 104 18 33.3 141 7 ADD06198 Add06198 Novel hum
 105 18 33.3 141 7 ADC77717 Adc77717 Novel hum
 106 18 33.3 141 7 ADD50680 Add50680 Novel hum
 107 18 33.3 141 7 ADD50926 Add50926 Novel hum
 108 18 33.3 141 7 ADD50407 Add50407 Human PRO
 109 18 33.3 141 7 ADD50161 Add50161 Human PRO
 110 18 33.3 141 7 ADD51172 Add51172 Novel hum
 111 18 33.3 141 7 ADI21041 Adi21041 Novel hum
 112 18 33.3 141 7 ADM03955 Adm03955 Human pro
 113 18 33.3 141 7 ADM10884 Adm10884 Human ova
 114 18 33.3 141 8 ADC48719 Adc48719 Novel hum
 115 18 33.3 141 8 ADE20890 Ade20890 Novel hum
 116 18 33.3 141 8 ADE05734 Ade05734 Human PRO
 117 18 33.3 141 8 ADD74963 Add74963 Human PRO
 118 18 33.3 141 8 ADD75709 Add75709 Novel hum
 119 18 33.3 141 8 ADD84941 Add84941 Novel hum
 120 18 33.3 141 8 ADD86767 Add86767 Novel hum
 121 18 33.3 141 8 ADE20644 Ade20644 Novel hum
 122 18 33.3 141 8 ADE38941 Ade38941 Novel hum
 123 18 33.3 141 8 ADE05488 Ade05488 Human PRO
 124 18 33.3 141 8 ADD73473 Add73473 Human PRO
 125 18 33.3 141 8 ADD78313 Add78313 Novel hum
 126 18 33.3 141 8 ADE21136 Ade21136 Novel hum
 127 18 33.3 141 8 ADD77251 Add77251 Novel hum
 128 18 33.3 141 8 ADE20398 Ade20398 Novel hum
 129 18 33.3 141 8 ADD75463 Add75463 Human PRO
 130 18 33.3 141 8 ADD73979 Add73979 Human PRO
 131 18 33.3 141 8 ADD74225 Add74225 Human PRO
 132 18 33.3 141 8 ADD75955 Add75955 Novel hum
 133 18 33.3 141 8 ADD85447 Add85447 Novel hum
 134 18 33.3 141 8 ADE04996 Ade04996 Human PRO
 135 18 33.3 141 8 ADD75209 Add75209 Human PRO
 136 18 33.3 141 8 ADD76753 Add76753 Novel hum
 137 18 33.3 141 8 ADD86521 Add86521 Novel hum
 138 18 33.3 141 8 ADD77989 Add77989 Novel hum
 139 18 33.3 141 8 ADD77497 Add77497 Novel hum
 140 18 33.3 141 8 ADD77743 Add77743 Novel hum
 141 18 33.3 141 8 ADD85201 Add85201 Novel hum
 142 18 33.3 141 8 ADD73733 Add73733 Human PRO
 143 18 33.3 141 8 ADD74471 Add74471 Human PRO
 144 18 33.3 141 8 ADD76999 Add76999 Novel hum
 145 18 33.3 141 8 ADD85693 Add85693 Novel hum
 146 18 33.3 141 8 ADE05242 Ade05242 Human PRO
 147 18 33.3 141 8 ADD74717 Add74717 Human PRO
 148 18 33.3 141 8 ADG05529 Adg05529 Novel hum
 149 18 33.3 141 8 ADG27083 Adg27083 Human PRO
 150 18 33.3 141 8 ADG11146 Adg11146 Novel hum

ALIGNMENTS

RESULT 1
 ID ABO23576 standard; protein; 103 AA.
 XX
 AC ABO23576;
 XX
 DT 04-SEP-2003 (first entry)
 XX
 DE Mycoplasma pneumoniae outlier protein #4.
 KW Candidate protein identification; pathogen; anti-infective;
 KW outlier protein; virulence protein; antigen; drug target protein;
 KW pathogenic organism; antimicrobial.
 XX Mycoplasma pneumoniae.
 XX

PN US2003039963-A1.
 XX 27-FEB-2003.
 PD 30-MAR-2001; 2001US-00820843.
 XX 30-MAR-2001; 2001US-00820843.
 XX (BRAH/) BRAHMACHARI S K.
 PA (RAMA/) RAMACHANDRAN S.
 PA (NAND/) NANDI T.
 PA (BHIM/) BHIMARAO C.
 XX Brahmachari SK, Ramachandran S, Nandi T, Bhimmarao C;
 PI WPI; 2003-492159/46.
 XX
 DR Identifying candidate proteins useful as anti-infectives involves
 XX matching outlier protein sequences with protein sequences in databases.
 XX
 PS Example 7; Page 78; 117pp; English.
 XX
 CC The present invention relates to a method for identifying candidate
 CC proteins in pathogens useful as anti-infectives. The invention discloses
 CC a computational method which involves the calculation of several sequence
 CC attributes and their subsequent analysis results in the identification
 CC of outlier proteins in different pathogens. The method is useful for the
 CC identification of outlier proteins (e.g. virulence proteins, antigens or
 CC proteins used as drug targets) in pathogenic organisms. The method of the
 CC invention provides reproducible results as it does not depend on the
 CC variable biochemical characterisation of proteins. ABO23500-ABO23617
 CC represent outlier proteins identified from different pathogenic organisms
 XX
 SQ Sequence 103 AA;
 XX
 Qy Query Match 35.2%; Score 19; DB 7; Length 103;
 Db Best Local Similarity 13.6%; Pred. No. 1.2e+04;
 XX Matches 3; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 Qy 3 CXXXXXXCXXXXXXCXXXXXXH 24
 Db 53 CSSISFCSLASSARLYRSSH 74
 XX
 RESULT 2
 ID AAW65945 standard; peptide; 10 AA.
 XX
 AC AAW65945;
 XX
 DT 12-NOV-1998 (first entry)
 XX
 DE Molecule V.
 XX
 KW Neurotrophin; cyclic; bicyclic; disulphide; nerve growth factor; NGF;
 KW BDNF; NT-3; conformation; promoter.
 XX
 OS Synthetic.
 OS Mammalia.
 XX
 PN CA2205045-AA.
 XX
 PD 12-MAY-1998.
 XX
 PF 09-MAY-1997; 97CA-02205045.
 XX
 PR 12-NOV-1996; 96CA-02190296.
 XX
 PA (TOOH) UNIV QUEENS KINGSTON.
 XX
 PI Riopelle RJ, Dory MI, Shamovsky IL, Weaver DF, Ross GM;
 XX WPI; 1998-457650/40.
 XX DR


```
XX OS Homo sapiens.
XX PN WO200142277-A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB004776.
XX PR 13-DEC-1999; 99GB-00029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WPI; 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX PS Example 4; Page 389; 646pp; English.
XX CC The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX SQ Sequence 10 AA;
Query Match 33.3%; Score 18; DB 4; Length 10;
Best Local Similarity 28.6%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
DB 4 CSSSTTC 10
RESULT 7
AAG96349
ID AAG96349 standard; peptide; 10 AA.
XX AC AAG96349;
XX DT 18-SEP-2001 (first entry)
XX DE Human complementary peptide, SEQ ID NO: 2543.
XX KW Human; complementary peptide; ligand; drug discovery; drug design.
XX OS Homo sapiens.
XX PN WO200142277-A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB004776.
XX PR 13-DEC-1999; 99GB-00029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WPI; 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX PS Example 4; Page 406; 646pp; English.
XX CC The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX SQ Sequence 10 AA;
Query Match 33.3%; Score 18; DB 4; Length 10;
Best Local Similarity 28.6%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
DB 4 CSSSTTC 10
RESULT 6
AAG96205
ID AAG96205 standard; peptide; 10 AA.
XX AC AAG96205;
XX DT 18-SEP-2001 (first entry)
XX DE Human complementary peptide, SEQ ID NO: 2399.
XX KW Human; complementary peptide; ligand; drug discovery; drug design.
XX OS Homo sapiens.
XX PN WO200142277-A2.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB004776.
XX PR 13-DEC-1999; 99GB-00029464.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WPI; 2001-408419/43.
XX A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
```

RESULT 8
 AAG96191
 ID AAG96191 standard; peptide; 10 AA.
 XX
 AC AAG96191;
 XX
 DT 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide, SEQ ID NO: 2385.
 XX
 KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX
 OS Homo sapiens.
 XX
 PN WO200142277-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 13-DEC-2000; 2000WO-GB004776.
 XX
 PR 13-DEC-1999; 99GB-00029464.
 XX
 PA (PROT-) PROTEOM LTD.
 XX
 PI Roberts GW, Heal JR;
 XX
 DR WPI; 2001-408419/43.
 XX
 A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX
 Example 4; Page 383; 646pp; English.
 XX
 The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification
 CC
 SQ Sequence 10 AA;
 Query Match 33.3%; Score 18; DB 4; Length 10;
 Best Local Similarity 28.6%; Pred. NO. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 3 CSSSTTC 9
 RESULT 9
 AAG96339
 ID AAG96339 standard; peptide; 10 AA.
 XX
 AC AAG96339;
 XX
 DT 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide, SEQ ID NO: 2533.
 XX
 KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX
 OS Homo sapiens.
 XX
 PN WO200142277-A2.
 XX
 PD 14-JUN-2001.
 XX
 A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX
 Example 4; Page 383; 646pp; English.
 XX
 The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification
 CC
 SQ Sequence 10 AA;
 Query Match 33.3%; Score 18; DB 4; Length 10;
 Best Local Similarity 28.6%; Pred. NO. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 3 CSSSTTC 9

PF 13-DEC-2000; 2000WO-GB004776.
 XX
 PR 13-DEC-1999; 99GB-00029464.
 XX
 PA (PROT-) PROTEOM LTD.
 XX
 PI Roberts GW, Heal JR;
 XX
 DR WPI; 2001-408419/43.
 XX
 A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX
 Example 4; Page 404; 646pp; English.
 XX
 The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification
 CC
 SQ Sequence 10 AA;
 Query Match 33.3%; Score 18; DB 4; Length 10;
 Best Local Similarity 28.6%; Pred. NO. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 2 CSSSTTC 8
 RESULT 10
 AAG96363
 ID AAG96363 standard; peptide; 10 AA.
 XX
 AC AAG96363;
 XX
 DT 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide, SEQ ID NO: 2557.
 XX
 KW Human; complementary peptide; ligand; drug discovery; drug design.
 XX
 OS Homo sapiens.
 XX
 PN WO200142277-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 13-DEC-2000; 2000WO-GB004776.
 XX
 PR 13-DEC-1999; 99GB-00029464.
 XX
 PA (PROT-) PROTEOM LTD.
 XX
 PI Roberts GW, Heal JR;
 XX
 DR WPI; 2001-408419/43.
 XX
 A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX
 Example 4; Page 408; 646pp; English.
 XX
 The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as

CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification

SQ Sequence 10 AA;

Query Match 33.3%; Score 18; DB 4; Length 10;
 Best Local Similarity 28.6%; Pred. No. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
 |
 Db 2 CSSSTTC 8

RESULT 11

AAG96333
 ID AAG96333 standard; peptide; 10 AA.

XX AC AAG96333;

XX DT 18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 2527.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB004776.

XX PR 13-DEC-1999; 99GB-00029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX DR WPI; 2001-408419/43.

XX PT A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX PS Example 4; Page 403; 646pp; English.

XX CC The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification

XX SQ Sequence 10 AA;

Query Match 33.3%; Score 18; DB 4; Length 10;
 Best Local Similarity 28.6%; Pred. No. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
 |
 Db 2 CSSSTTC 8

RESULT 12

AAG96193

ID AAG96193 standard; peptide; 10 AA.

XX AC AAG96193;

XX DT

18-SEP-2001 (first entry)

XX DE Human complementary peptide, SEQ ID NO: 2387.

XX KW Human; complementary peptide; ligand; drug discovery; drug design.

XX OS Homo sapiens.

XX PN WO200142277-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB004776.

XX PR 13-DEC-1999; 99GB-00029464.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX DR WPI; 2001-408419/43.

XX PT A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX PS Example 4; Page 384; 646pp; English.

XX CC The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification

XX SQ Sequence 10 AA;

Query Match 33.3%; Score 18; DB 4; Length 10;
 Best Local Similarity 28.6%; Pred. No. 6.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXXC 9
 |
 Db 4 CSSSTTC 10

RESULT 13

AAW54432

ID AAW54432 standard; peptide; 12 AA.

XX AC AAW54432;

XX DT 15-SEP-1998 (first entry)

XX DE Human PS112 protein synthetic peptide #7.

XX KW Prostate; disease; PS112 gene; detection; diagnosis; cancer; treatment;
 KW antibody.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9815657-A1.

XX PD 16-APR-1998.

XX PF 08-OCT-1997; 97WO-US018290.

XX PR 08-OCT-1996; 96US-00727688.

XX PA (ABRO) ABBOTT LAB.

XX Cohen M, Friedman PN, Gordon J, Hodges SC, Klaas MR;
 PI Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD;
 XX WPI; 1998-240838/21.
 XX Detecting a target PS112 polynucleotide - used for diagnosing prostate
 PT cancer.
 XX Example 10; Page 92; 104pp; English.
 XX AAW54426-W54433 represent synthetic peptide fragments of designed from
 CC the human PS112 protein isolated from a prostate library. These peptides
 CC are used in a novel method of detecting the presence of a target PS112
 CC polynucleotide in a test sample. The method can also be used to detect
 CC mRNA of PS112 in a test sample. The method can be used for diagnosis of
 CC prostate cancer, as the presence of PS112 is an indicator of prostate
 CC cancer. Antibodies against the polypeptides may be used as markers, or to
 CC treat prostate cancer
 XX Sequence 12 AA;
 Query Match 33.3%; Score 18; DB 2; Length 12;
 Best Local Similarity 28.6%; Pred. No. 6.7e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 1 CSSSSSC 7
 RESULT 14
 ID AAB08422 standard; peptide; 12 AA.
 XX AAB08422;
 AC AAB08422;
 DT 20-DEC-2000 (first entry)
 XX Antigen peptide derived from prostate cancer associated protein PS112.
 XX Prostate cancer associated gene; PS112; prostate disease;
 KW prostate cancer; tumour; metastasis.
 XX Synthetic.
 OS Homo sapiens.
 XX US6110675-A.
 PN 29-AUG-2000.
 PD 08-OCT-1997; 97US-00946869.
 PF 08-OCT-1996; 96US-00727688.
 PR (ABBO) ABBOTT LAB.
 XX Friedman PN, Gordon J, Hodges SC, Klaas MR, Cohen M;
 PI Roberts-Rapp L, Russell JC, Stroupe SD, Yu H, Kratochvil JD;
 XX WPI; 2000-571422/53.
 XX Novel methods for diagnosing prostate cancer by contacting test sample
 PT with target specific polynucleotide and detecting prostate cancer
 PT associated polynucleotides.
 XX Example 10; Col 77-78; 50pp; English.
 XX AAB08416-23 represent antigenic peptides derived from a protein which is
 CC encoded by a human prostate cancer associated gene, designated PS112. The
 CC peptides are used to raise antibodies. PS112 sequences are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, preventing,
 CC treating, or determining the predisposition of an individual to disease

CC and conditions of the prostate, such as prostate cancer, tumours and
 CC metastases
 XX Sequence 12 AA;
 Query Match 33.3%; Score 18; DB 3; Length 12;
 Best Local Similarity 28.6%; Pred. No. 6.7e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 DB 1 CSSSSSC 7
 RESULT 15
 ID ADQ96644 standard; peptide; 12 AA.
 XX ADQ96644;
 AC ADQ96644;
 DT 23-SEP-2004 (first entry)
 XX Human PS112 epitope seqid 32.
 DE cytostatic; gene therapy; PS112; recombinant expression system;
 KW PS112 epitope; prostate disease; tumours; metastasis; predisposition;
 KW prostate cancer; epitope.
 XX Synthetic.
 OS US2004121397-A1.
 PN 24-JUN-2004.
 PD 22-JAN-2004; 2004US-00763992.
 PF 08-OCT-1996; 96US-00727688.
 PR 08-OCT-1997; 97US-00946869.
 PR 15-OCT-1999; 99US-00418887.
 XX (COHE/) COHEN M.
 PA (FRIE/) FRIEDMAN P N.
 PA (GORD/) GORDON J.
 PA (HODG/) HODGES S C.
 PA (KLAS/) KLAAS M R.
 PA (KRAT/) KRATOCHVIL J D.
 PA (ROBE/) ROBERTS-RAPP L.
 PA (RUSS/) RUSSELL J C.
 PA (STRO/) STROUPE S D.
 PA (YUHH/) YU H.
 XX Cohen M, Friedman PN, Gordon J, Hodges SC, Klaas MR;
 PI Kratochvil JD, Roberts-Rapp L, Russell JC, Stroupe SD, Yu H;
 XX WPI; 2004-479676/45.
 XX Detecting a target PS112 polynucleotide, useful in diagnosing, staging,
 PT monitoring, prognosticating, preventing and treating prostate cancer,
 PT comprises contacting the test sample with PS112-specific polynucleotide.
 XX Example 10; SEQ ID NO 32; 53pp; English.
 XX The invention describes a method of detecting the presence of a target
 CC PS112 polynucleotide in a test sample. The method comprises: contacting
 CC the test sample with at least one PS112-specific polynucleotide or its
 CC complement; and detecting the presence of the target PS112 polynucleotide
 CC in the test sample, where the PS112-specific polynucleotide has at least
 CC 50% identity to a polynucleotide comprising a sequence of 367, 214, 205,
 CC 256, 246, 277, 251, 223, 2393, or 1297 bp (SEQ ID NOS: 1-10) or their
 CC fragments or complements. Also described are: detecting mRNA of PS112 in
 CC a test sample; a test kit, useful for detecting PS112 polynucleotide in
 CC test sample; a purified polynucleotide or fragment derived from a PS112
 CC gene; a recombinant expression system comprising a nucleic acid sequence

CC that includes an open reading frame derived from P8112 operably linked to
 CC a control sequence compatible with a desired host, where the nucleic acid
 CC sequence has at least 50% identity to a sequence of SEQ ID NOS: 1-10, or
 CC their fragments or complements; a cell transfected with the recombinant
 CC expression system or with a nucleic acid sequence encoding at least one
 CC P8112 epitope, where the nucleic acid sequence comprises SEQ ID NOS: 1-
 CC 10, or their fragments or complements; a composition of matter comprising
 CC a P8112 polynucleotide or its fragment, where the polynucleotide has at
 CC least 50% identity to a sequence of SEQ ID NOS: 2-10, or their
 CC complements, or has at least 50% identity with fragments of a
 CC polynucleotide of SEQ ID NOS: 4-8; and a gene or its fragment comprising
 CC DNA having at least 50% identity with SEQ ID NOS: 9 or 10. The method is
 CC useful for detecting the presence of a target P8112 polynucleotide in a
 CC test sample. The methods, test kit, polynucleotides and polypeptides, and
 CC antibodies are useful in detecting, diagnosing, staging, monitoring, or
 CC prognosticating, preventing and treating prostate diseases, tumours or
 CC metastases or in determining the predisposition of an individual to
 CC diseases and conditions of the prostate, e.g. prostate cancer. This is
 CC the amino acid sequence of a P8112 epitope used in the creation of anti-
 CC P8112-antibodies.

XX SQ Sequence 12 AA;
 Query Match 33.3%; Score 18; DB 8; Length 12;
 Best Local Similarity 28.6%; Pred. No. 6.7e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CXXXXXC 9
 Db 1 CXXXXXC 7

RESULT 16
 AAR97928
 ID AAR97928 standard; peptide; 15 AA.

XX AC AAR97928;
 XX DT 16-AUG-1996 (first entry)
 XX DE Japan cedar pollen mature allergen Cry j II amino acids 286-300.
 XX KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 XX KW Sugi pollinosis; diagnosis; treatment.
 XX OS Cryptomeria japonica.

XX PN JP08047392-A.
 XX PD 20-FEB-1996.
 XX PF 07-NOV-1994; 94JP-00297840.
 XX PR 05-NOV-1993; 93JP-00276773.
 XX PR 26-MAY-1994; 94JP-00134868.
 XX PA (MEIP) MEIJI MILK PROD CO LTD.
 XX DR WPI; 1996-166249/17.

PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of
 PT specified 460 aminoacid protein.

PS Disclosure; Fig 5; 17pp; Japanese.
 XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
 CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment of
 CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
 CC regions of the allergen were identified using the overlapping peptides of
 CC the full epitope derived from a Cry j II antigen-specific T cell line.
 CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
 CC amino acid allergen are the most allergenic of the 90 peptides tested

XX SQ Sequence 15 AA;
 Query Match 33.3%; Score 18; DB 2; Length 15;
 Best Local Similarity 28.6%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CXXXXXC 9
 Db 8 CTSASAC 14

RESULT 17
 AAR97929
 ID AAR97929 standard; peptide; 15 AA.

XX AC AAR97929;
 XX DT 16-AUG-1996 (first entry)
 XX DE Japan cedar pollen mature allergen Cry j II amino acids 291-310.
 XX KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 XX KW Sugi pollinosis; diagnosis; treatment.
 XX OS Cryptomeria japonica.

XX PN JP08047392-A.
 XX PD 20-FEB-1996.
 XX PF 07-NOV-1994; 94JP-00297840.
 XX PR 05-NOV-1993; 93JP-00276773.
 XX PR 26-MAY-1994; 94JP-00134868.

XX PA (MEIP) MEIJI MILK PROD CO LTD.
 XX DR WPI; 1996-166249/17.

XX DE Japan cedar pollen allergen Cry j II epitope - comprises at least part of
 PT specified 460 aminoacid protein.
 XX PS Disclosure; Fig 5; 17pp; Japanese.
 XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of
 CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment of
 CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
 CC regions of the allergen were identified using the overlapping peptides of
 CC the full epitope derived from a Cry j II antigen-specific T cell line.
 CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
 CC amino acid allergen are the most allergenic of the 90 peptides tested

XX SQ Sequence 15 AA;
 Query Match 33.3%; Score 18; DB 2; Length 15;
 Best Local Similarity 28.6%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 CXXXXXC 9
 Db 3 CTSASAC 9

RESULT 18
 ABP83105
 ID ABP83105 standard; peptide; 18 AA.

XX AC ABP83105;
 XX DT 04-MAR-2003 (first entry)
 XX DR

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1778.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burmer GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Claim 1; Fig 2; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX

SQ Sequence 18 AA;

Query Match 33.3%; Score 18; DB 6; Length 18;
 Best Local Similarity 28.6%; Pred. No. 8.1e+03;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
 DB 9 CASSSSC 15

RESULT 19

AAW42192

ID AAW42192 standard; peptide; 20 AA.

XX AC AAW42192;

XX DT 27-AUG-2003 (revised)

XX DT 25-MAR-2003 (revised)

XX DT 16-JUN-1998 (first entry)

XX T-cell epitope peptide 72 from Japanese cypress pollen antigen Chao2.
 XX Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
 KW diagnosis; allergy; spring tree pollen disease; pollinosis.
 XX Chamaecyparis obtusa.
 XX WO9747648-A1.
 XX PD 18-DEC-1997.
 XX PF 12-JUN-1997; 97WO-JP002031.
 XX PR 14-JUN-1996; 96JP-00153527.
 XX (MEIP) MEIJI MILK PROD CO LTD.
 XX Kino K, Dairiri K;
 XX WPI; 1998-052242/05.
 XX T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
 PT and Chao2 - used for diagnosis and treatment of spring tree pollen
 PT disease.
 XX Claim 2; Page 48; 71pp; Japanese.

XX The present sequence represents a T-cell epitope peptide from Japanese
 CC cypress pollen antigen Chao2. The present invention describes peptides
 CC which correspond to the T-cell epitope sites on Japanese cypress pollen
 CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
 CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
 CC treatment and prevention of spring tree pollen disease in which the
 CC pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
 CC -MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX Sequence 20 AA;
 SQ

Query Match 33.3%; Score 18; DB 2; Length 20;

Best Local Similarity 28.6%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9

DB 7 CTSASAC 13

RESULT 20

ADM10961

ID ADM10961 standard; peptide; 25 AA.

XX AC ADM10961;

XX DT 20-MAY-2004 (first entry)

XX DE Human ovary-specific O1034C/O591S peptide #2.

XX KW ovarian; tumour protein; cancer; T cell; CD4+ cell; CD8+ cell;
 KW cystostatic; gene therapy; human; ds.
 XX Homo sapiens.

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XX US2003206918-A1.
XX
XX PD 06-NOV-2003.
XX
XX PF 05-FEB-2003; 2003US-00361811.
XX
XX PR 10-SEP-1999; 99US-00394374.
XX PR 01-MAY-2000; 2000US-00561778.
XX PR 15-AUG-2000; 2000US-00640173.
XX PR 07-SEP-2000; 2000US-00656668.
XX PR 14-NOV-2000; 2000US-00713550.
XX PR 03-APR-2001; 2001US-00825294.
XX PR 02-OCT-2001; 2001US-00970966.
XX PR 02-AUG-2002; 2002US-00212677.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Fanger GR, Fling SP;
XX
XX DR WPI; 2003-901037/82.
XX
XX PT New polynucleotides encoding tumor proteins, treating or inhibiting the
XX PT development of cancer, particularly ovarian cancer, and for stimulating
XX PT and/or expanding T cells specific for a tumor protein.
XX
XX PS Claim 2; SEQ ID NO 292; 221pp; English.
XX
XX CC This invention describes a novel ovarian tumour protein which can be used
XX CC to detecting the presence of an ovarian cancer in a patient by
XX CC stimulating and/or expanding T cells specific for the tumour protein. The
XX CC products of the invention can also be used in a method to inhibit the
XX CC development of a cancer in a patient comprising (a) incubating CD4+
XX CC and/or CD8+ T cells isolated from a patient with at least one ovarian
XX CC tumour protein, such that T cell proliferate and (b) administering to the
XX CC patient the proliferated T cells. The cytostatic polynucleotides or
XX CC polypeptides described in the invention are useful for treating or
XX CC inhibiting the development of cancer, particularly ovarian cancer and for
XX CC stimulating and/or expanding T cells specific for a tumour protein or for
XX CC gene therapy.
XX
XX SQ Sequence 25 AA;
XX
XX Query Match 33.3%; Score 18; DB 7; Length 25;
XX Best Local Similarity 28.6%; Pred. No. 9.5e+03;
XX Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 3 CXXXXXC 9
XX DB 18 CASSAAC 24
XX
XX RESULT 21
XX ADJ11291
XX ID ADJ11291 standard; peptide; 25 AA.
XX
XX XX
XX AC ADJ11291;
XX
XX DT 15-APR-2004 (first entry)
XX
XX DE Rabbit anti-human peptide against an ovarian tumour antigen SeqID 292.
XX
XX KW ovarian cancer; immunogenic; antibody; antigen presenting cell; APC;
XX KW immune system cell; T cell; tumourigenic; cytostatic; antibody; rabbit.
XX
XX OS Oryctolagus cuniculus.
XX OS Synthetic.
XX
XX PN US2003232056-A1.
XX
XX PD 18-DEC-2003.
XX
XX PF 14-FEB-2003; 2003US-00369186.

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XX 10-SEP-1999; 99US-00394374.
XX PR 01-MAY-2000; 2000US-00561778.
XX PR 15-AUG-2000; 2000US-00640173.
XX PR 07-SEP-2000; 2000US-00656668.
XX PR 14-NOV-2000; 2000US-00713550.
XX PR 03-APR-2001; 2001US-00825294.
XX PR 02-OCT-2001; 2001US-00970966.
XX PR 02-AUG-2002; 2002US-00212677.
XX PR 05-FEB-2003; 2003US-00361811.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Fanger GR, Fling SP;
XX
XX DR WPI; 2004-178717/17.
XX
XX PT Novel isolated ovarian tumor polynucleotide encoding ovarian tumor
XX PT polypeptide, useful as probes of primers for detecting presence of cancer
XX PT in a patient.
XX
XX PS Claim 2; SEQ ID NO 292; 222pp; English.
XX
XX CC This invention relates to novel isolated polynucleotides and methods for
XX CC the therapy and diagnosis of cancer, particularly ovarian cancer.
XX CC Specifically, it refers to these polynucleotides and the encoded
XX CC polypeptides thereof, as well as immunogenic peptides, antibodies,
XX CC antigen presenting cells (APCs) and immune system cells (e.g. T cells)
XX CC that are targeted to those cells expressing the proteins of interest. The
XX CC present invention describes methods that are useful for stimulating and/or
XX CC expanding T cells specific for a tumourigenic protein (i.e. T cell
XX CC therapy). Furthermore, compositions can be used for the diagnosis,
XX CC treatment and/or prevention of ovarian cancer by stimulating an immune
XX CC response in a patient. Accordingly, these compositions exhibit cytostatic
XX CC activity. This peptide is a synthetic peptide used for generation of
XX CC rabbit polyclonal anti-sera used against human ovarian tumour antigen
XX CC sequences given in an exemplification of the invention.
XX
XX SQ Sequence 25 AA;
XX
XX Query Match 33.3%; Score 18; DB 8; Length 25;
XX Best Local Similarity 28.6%; Pred. No. 9.5e+03;
XX Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 3 CXXXXXC 9
XX DB 18 CASSAAC 24
XX
XX RESULT 22
XX ABB42303
XX ID ABB42303 standard; peptide; 28 AA.
XX
XX AC ABB42303;
XX
XX DT 04-FEB-2002 (first entry)
XX
XX DE Peptide #9809 encoded by human foetal liver single exon probe.
XX
XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
XX OS Homo sapiens.
XX
XX PN WO200157277-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US000669.
XX
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.

```

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX Claim 27; SEQ ID NO 34938; 639pp + Sequence Listing; English.
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 28 AA;
 SQ Query Match 33.3%; Score 18; DB 4; Length 28;
 Best Local Similarity 28.6%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 Db 3 CASSSAC 9
 RESULT 23
 ID AAM36111 standard; protein; 28 AA.
 XX AAM36111;
 XX 17-OCT-2001 (first entry)
 DT Peptide #10148 encoded by probe for measuring placental gene expression.
 DE Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 KW Homo sapiens.
 OS WO200157272-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US000663.
 PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 36380; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX Sequence 28 AA;
 SQ Query Match 33.3%; Score 18; DB 4; Length 28;
 Best Local Similarity 28.6%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 3 CXXXXXC 9
 Db 3 CASSSAC 9
 RESULT 24
 ID ABB25806 standard; protein; 28 AA.
 XX ABB25806;
 XX 23-JAN-2002 (first entry)
 DT Protein #7805 encoded by probe for measuring heart cell gene expression.
 DE Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX Homo sapiens.
 OS WO200157274-A2.
 PN 09-AUG-2001.
 PD 30-JAN-2001; 2001WO-US000666.
 PF 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX Claim 15; SEQ ID NO 27576; 530pp; English.
 PS The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hyperextension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

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XX SQ Sequence 28 AA;
Query Match 33.3%; Score 18; DB 4; Length 28;
Best Local Similarity 28.6%; Pred. NO. 1e+04;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 3 CASSSAC 9

RESULT 25
AAM76003
ID AAM76003 standard; protein; 28 AA.
XX AC
XX AC AAM76003;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36309.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
XX KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX DR Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 36309; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is a
XX CC protein encoded by one of the probes of the invention
XX SQ Sequence 28 AA;
Query Match 33.3%; Score 18; DB 4; Length 28;
Best Local Similarity 28.6%; Pred. NO. 1e+04;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 3 CASSSAC 9

RESULT 26
AAM63189
ID AAM63189 standard; protein; 28 AA.
XX AC
XX AC AAM63189;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35294.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
XX KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX DR Single exon nucleic acid probes for analyzing gene expression in human
XX PT brains.
XX PS Example 4; SEQ ID NO 35294; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC brain. They can be used to measure gene expression in brain cell samples,
XX CC which may enable the diagnosis and improved treatment of nervous system
XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, of
XX CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX CC the probes of the invention
XX SQ Sequence 28 AA;
Query Match 33.3%; Score 18; DB 4; Length 28;
Best Local Similarity 28.6%; Pred. NO. 1e+04;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 3 CASSSAC 9

RESULT 27
ABG57729
ID ABG57729 standard; peptide; 28 AA.
XX AC
XX AC ABG57729;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID NO 36377.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN WO200157273-A2.
XX
```

PD 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000664.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 XX Claim 27; SEQ ID NO 36377; 658pp; English.
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridizes at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinemia, hyperlipidemia and hypercholesterolemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 28 AA;
 SQ
 Query Match 33.3%; Score 18; DB 4; Length 28;
 Best Local Similarity 28.6%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 CXXXXXC 9
 Db 3 CASSSAC 9
 RESULT 28
 ABG45410
 ID ABG45410 standard; peptide; 28 AA.
 XX AC ABG45410;
 XX 19-AUG-2002 (first entry)
 DT Human peptide encoded by genome-derived single exon probe SEQ ID 35075.
 DE Human; single exon probe; asthma; lung cancer; COPD; ILD;
 XX chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX Homo sapiens.
 OS WO200196003-A2.
 XX PN
 XX

PD 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US000665.
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX Claim 27; SEQ ID NO 35075; 634pp; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridize at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 28 AA;
 SQ
 Query Match 33.3%; Score 18; DB 5; Length 28;
 Best Local Similarity 28.6%; Pred. No. 1e+04;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 CXXXXXC 9
 Db 3 CASSSAC 9

RESULT 29

ABO57875
XX ID ABO57875 standard; protein; 39 AA.
XX AC ABO57875;
XX DT 29-JUL-2004 (first entry)
XX DE Human genome derived single exon protein #4109.
XX DE Human; gene expression; single exon probe; microarray;
XX KW alternative splicing event; genomic alteration.
XX OS Homo sapiens.
XX PN US2003194704-A1.
XX PD 16-OCT-2003.
XX PF 03-APR-2002; 2002US-00029386.
XX PR 03-APR-2002; 2002US-00029386.
XX PA (PENN/) PENN S G.
XX PA (RANK/) RANK D R.
XX PA (HANZ/) HANZEL D K.
XX PI Penn SG, Rank DR, Hanzel DK;
XX DR WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX Claim 45; SEQ ID NO 31509; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridises under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subscription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterising
XX alternative splicing events, in detecting and characterising gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in priming the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe protein of the invention. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030194704

XX
SQ

Sequence 39 AA;

Query Match 33.3%; Score 18; DB 8; Length 39;
Best Local Similarity 28.6%; Pred. NO. 1.2e+04;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
|
Db 19 CSATSTC 25

RESULT 30

ABG05767
ID ABG05767 standard; protein; 57 AA.
XX AC ABG05767;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #5758.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS69954.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.

Claim 20; SEQ ID NO 36126; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ

Sequence 57 AA;

Query Match 33.3%; Score 18; DB 4; Length 57;
Best Local Similarity 28.6%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
Db 46 CSTSASC 52

Search completed: April 27, 2005, 16:44:29
Job time : 172 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	19	35.2		103	2	S73440	hypothetical prote
2	18	33.3		121	1	RWBEM3	surface glycoprote
3	18	33.3		135	2	A45835	ly6 homolog RK10 p
4	18	33.3		157	2	S09805	hypothetical prote
5	18	33.3		295	2	T00399	probable AP2 domai
6	18	33.3		381	2	B97542	hypothetical prote
7	18	33.3		381	2	AD2761	rare lipoprotein A
8	18	33.3		404	2	JCS784	adrenomedullin rec
9	18	33.3		442	2	T21196	hypothetical prote
10	18	33.3		492	2	S49147	ERF-2 protein - hu
11	18	33.3		507	2	JC3766	Jun a 2 protein -
12	18	33.3		514	2	S48730	Cry j II protein -
13	18	33.3		514	2	JC2498	second major aller
14	18	33.3		514	2	JCT100	polygalacturonase
15	18	33.3		525	2	IS3194	cdc25A - rat
16	18	33.3		584	1	C8HUA	complement C8 alph
17	18	33.3		675	2	D48492	kpsC protein - Esc
18	18	33.3		746	2	T24978	hypothetical prote
19	18	33.3		1817	2	T34249	hypothetical prote
20	17	31.5		25	1	SNWR	metallothionein -
21	17	31.5		26	1	SMNC	metallothionein -
22	17	31.5		26	2	S55029	CAP3 protein - ant
23	17	31.5		27	2	S42359	ferredoxin [3Fe-4S
24	17	31.5		45	1	FFYZ	fulvicoin C - Myxoc
25	17	31.5		45	2	AC3539	hypothetical prote
26	17	31.5		61	1	SMHY1C	metallothionein I
27	17	31.5		61	2	S00810	metallothionein Ic
28	17	31.5		66	2	S59621	metallothionein Ic
29	17	31.5		71	2	H95299	hypothetical prote

103 17 31.5 326 2 T27655
104 17 31.5 330 2 T39511
105 17 31.5 335 2 T32058
106 17 31.5 335 2 A39743
107 17 31.5 336 2 B71366
108 17 31.5 336 2 C69811
109 17 31.5 339 2 A95937
110 17 31.5 343 2 A37377
111 17 31.5 346 2 D42087
112 17 31.5 346 2 S64693
113 17 31.5 348 2 T40152
114 17 31.5 352 2 T42744
115 17 31.5 354 2 B97003
116 17 31.5 356 2 T19520
117 17 31.5 360 2 D84646
118 17 31.5 360 2 S69063
119 17 31.5 362 2 I37459
120 17 31.5 369 2 T38428
121 17 31.5 370 2 E70390
122 17 31.5 371 2 T27643
123 17 31.5 374 2 JC2123
124 17 31.5 374 2 JC2124
125 17 31.5 389 2 T34766
126 17 31.5 392 2 A60777
127 17 31.5 393 2 D70858
128 17 31.5 396 2 T45399
129 17 31.5 400 2 E88206
130 17 31.5 403 2 E87710
131 17 31.5 404 2 AH0803
132 17 31.5 404 2 JS0073
133 17 31.5 404 2 C97154
134 17 31.5 405 2 C83443
135 17 31.5 406 1 SYEAL1
136 17 31.5 406 2 G84940
137 17 31.5 406 2 G91029
138 17 31.5 406 2 H85873
139 17 31.5 406 2 A64128
140 17 31.5 407 2 AE0336
141 17 31.5 407 2 AH2594
142 17 31.5 410 2 F87122
143 17 31.5 412 1 KRSHL1
144 17 31.5 416 2 A45510
145 17 31.5 416 2 A61404
146 17 31.5 416 2 S60034
147 17 31.5 416 2 A46559
148 17 31.5 433 2 T02655
149 17 31.5 438 1 S70602
150 17 31.5 438 2 D88206

ALIGNMENTS

RESULT 1
S73440
Hypothetical protein B01_orf103b - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327, MUID:97105885, PMID:8948633
A:Accession: S73440
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-103 <HIM>
A:Cross-references: UNIPROT:P75074; EMBL:AE000014; GB:U00089; NID:g1673770; PIDN:AA89578
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3

Query Match 35.2%; Score 19; DB 2; Length 103;
Best Local Similarity 13.6%; Pred. No. 2.4e+02;
Matches 3; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 3 CXXXXXXCXXXXXXXXXXXXX 24
DB 53 CSSISFCSLASSARLRYSSSH 74
RESULT 2
RWBEM3
surface glycoprotein CD59 precursor homolog - saimirine herpesvirus 1 (strain 11)
C:Species: saimirine herpesvirus 1
A:Note: host Saimiri sciureus (common squirrel monkey)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
R:Albrecht, J.C.; Nicholas, J.; Cameron, K.R.; Newman, C.; Fleckenstein, B.; Honess, R.W.
C:Accession: A43384; F36807
Virology 190, 527-530, 1992
A:Title: Herpesvirus saimiri has a gene specifying a homologue of the cellular membrane
A:Reference number: A43384; MUID:92410640; PMID:1382344
A:Accession: A43384
A:Molecule type: DNA
A:Residues: 1-121 <ALB>
A:Cross-references: GB:S44811; GB:X64273; NID:G60318; PIDN:CAA45565.1; PID:G60319
C:Genetics:
A:Gene: 15
C:Superfamily: Ly-6 antigen; Ly-6 homology
C:Keywords: glycoprotein; lipoprotein; phosphatidylinositol linkage
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-96/Product: surface glycoprotein #status predicted <SGP>
F:20-96/Domain: Ly-6 homology <LY6>
F:97-121/Domain: carboxyl-terminal propeptide #status predicted <CPP>
F:24/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 33.3%; Score 18; DB 1; Length 121;
Best Local Similarity 28.6%; Pred. No. 4.8e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CXXXXXC 9
DB 32 CTTTSTSC 38
RESULT 3
A45835
Ly6 homolog RK10 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A45835; B45835
R:Friedman, S.; Palfrey, R.G.E.; Sirlin, S.; Haemmerling, U.
Immunogenetics 31, 104-111, 1990
A:Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidney
A:Reference number: A45835; MUID:90152758; PMID:2154400
A:Accession: A45835
A:Molecule type: mRNA
A:Residues: 1-135 <FRI>
A:Cross-references: UNIPROT:Q63317; GB:M30689; NID:G205247; PIDN:AAA41546.1; PID:G205248
A:Experimental source: clone RK10
A:Accession: B45835
A:Molecule type: mRNA
A:Residues: 25-54, 'A', 56-62, 'M', 64-67, 'Q', 69-71, 'DHI', 75-77, 'V', 79-80, 'T', 82-85, 'T', 87, 'V', 89-91, 'V', 93-95, 'V', 97-99, 'V', 101-103, 'V', 105-107, 'V', 109-111, 'V', 113-115, 'V', 117-119, 'V', 121-123, 'V', 125-127, 'V', 129-131, 'V', 133-135, 'V', 137-139, 'V', 141-143, 'V', 145-147, 'V', 149-151, 'V', 153-155, 'V', 157-159, 'V', 161-163, 'V', 165-167, 'V', 169-171, 'V', 173-175, 'V', 177-179, 'V', 181-183, 'V', 185-187, 'V', 189-191, 'V', 193-195, 'V', 197-199, 'V', 201-203, 'V', 205-207, 'V', 209-211, 'V', 213-215, 'V', 217-219, 'V', 221-223, 'V', 225-227, 'V', 229-231, 'V', 233-235, 'V', 237-239, 'V', 241-243, 'V', 245-247, 'V', 249-251, 'V', 253-255, 'V', 257-259, 'V', 261-263, 'V', 265-267, 'V', 269-271, 'V', 273-275, 'V', 277-279, 'V', 281-283, 'V', 285-287, 'V', 289-291, 'V', 293-295, 'V', 297-299, 'V', 301-303, 'V', 305-307, 'V', 309-311, 'V', 313-315, 'V', 317-319, 'V', 321-323, 'V', 325-327, 'V', 329-331, 'V', 333-335, 'V', 337-339, 'V', 341-343, 'V', 345-347, 'V', 349-351, 'V', 353-355, 'V', 357-359, 'V', 361-363, 'V', 365-367, 'V', 369-371, 'V', 373-375, 'V', 377-379, 'V', 381-383, 'V', 385-387, 'V', 389-391, 'V', 393-395, 'V', 397-399, 'V', 401-403, 'V', 405-407, 'V', 409-411, 'V', 413-415, 'V', 417-419, 'V', 421-423, 'V', 425-427, 'V', 429-431, 'V', 433-435, 'V', 437-439, 'V', 441-443, 'V', 445-447, 'V', 449-451, 'V', 453-455, 'V', 457-459, 'V', 461-463, 'V', 465-467, 'V', 469-471, 'V', 473-475, 'V', 477-479, 'V', 481-483, 'V', 485-487, 'V', 489-491, 'V', 493-495, 'V', 497-499, 'V', 501-503, 'V', 505-507, 'V', 509-511, 'V', 513-515, 'V', 517-519, 'V', 521-523, 'V', 525-527, 'V', 529-531, 'V', 533-535, 'V', 537-539, 'V', 541-543, 'V', 545-547, 'V', 549-551, 'V', 553-555, 'V', 557-559, 'V', 561-563, 'V', 565-567, 'V', 569-571, 'V', 573-575, 'V', 577-579, 'V', 581-583, 'V', 585-587, 'V', 589-591, 'V', 593-595, 'V', 597-599, 'V', 601-603, 'V', 605-607, 'V', 609-611, 'V', 613-615, 'V', 617-619, 'V', 621-623, 'V', 625-627, 'V', 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2909-2911, 'V', 2913-

Db 41 CSSTATC 47

RESULT 4

S09805

hypothetical protein UL42 - human cytomegalovirus (strain AD169)

C:Species: human cytomegalovirus, human herpesvirus 5

A:Note: host Homo sapiens (man)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S09805

R:Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;

M.; Barrall, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990

A:Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus

A:Reference number: S09749; MUID:90269039; PMID:2161319

A:Accession: S09805

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-157 <CHE>

A:Cross-references: UNIPROT:P16815; EMBL:X17403; NID:G59591; PIDN:CAA35401.1; PID:e27241

A:Note: this sequence was submitted to the EMBL Data Library, December 1989

A:Note: this reading frame extends between two stop codons and does not begin with a sta

C:Superfamily: human cytomegalovirus hypothetical protein UL42

C:Keywords: glycoprotein; transmembrane protein

F:117-143/Domain: transmembrane #status predicted

F:147/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 33.3%; Score 18; DB 2; Length 157;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9

Db 76 CAATSSC 82

RESULT 5

T00399

probable AP2 domain transcription factor [imported] - Arabidopsis thaliana

N:Alternate names: transcription factor TINY homolog T13E15.5

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00399; F84884

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Maso

submitted to the EMBL Data Library, July 1997

A:Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.

A:Reference number: Z14146

A:Accession: T00399

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-295 <ROU>

A:Cross-references: UNIPROT:Q22158; EMBL:AC002388; NID:g3420042; PID:g2344890

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: F84884

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-295 <STO>

A:Cross-references: GB:AE002093; NID:g4895256; PIDN:AAD32841.1; GSPDB:GN00139

C:Genetics:

A:Map position: 2

Query Match

Best Local Similarity 33.3%; Score 18; DB 2; Length 295;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9

Db 76 CAATSSC 82

RESULT 8

JC5784

adrenomedullin receptor - human

C:Species: Homo sapiens (man)

QY 3 CXXXXXC 9
Db 233 CASTSAC 239

RESULT 6

B97542

hypothetical protein AGR_C 2765 [imported] - Agrobacterium tumefaciens (strain C58, Cer:

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: B97542

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: B97542

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-381 <KUR>

A:Cross-references: UNIPROT:Q8UF98; GB:AE007869; PIDN:AAK87291.1; PID:g15156585; GSPDB:

C:Genetics:

A:Gene: AGR_C 2765

A:Map position: circular chromosome

C:Superfamily: rplA lipoprotein

Query Match

Best Local Similarity 33.3%; Score 18; DB 2; Length 381;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9

Db 44 CAATASC 50

RESULT 7

AD2761

rare lipoprotein A [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AD2761

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo;

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.;

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AD2761

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-381 <KUR>

A:Cross-references: UNIPROT:Q8UF98; GB:AE008688; PIDN:AAL42506.1; PID:g17739925; GSPDB:

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: rlpA

A:Map position: circular chromosome

C:Superfamily: rplA lipoprotein

Query Match

Best Local Similarity 33.3%; Score 18; DB 2; Length 381;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9

Db 44 CAATASC 50

C>Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: J05784
R:Haenze, J.; Dittlich, K.; Doetsch, J.; Rascher, W.
Biochem. Biophys. Res. Commun. 240, 183-188, 1997
A:Title: Molecular cloning of a novel human receptor gene with homology to the rat adreno-
A:Reference number: J05784; MUID:98042541; PMID:9367907
A:Accession: J05784
A:Molecule type: mRNA
A:Residues: 1-404 <HAE>
A:Cross-references: UNIPROT:O15218; GB:Y13583; NID:g2652933; PIDN:CAA73910.1; PID:g26529
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; receptor; transmembrane protein
F:58-79/Domain: transmembrane #status predicted <TM1>
F:91-113/Domain: transmembrane #status predicted <TM2>
F:128-149/Domain: transmembrane #status predicted <TM3>
F:171-193/Domain: transmembrane #status predicted <TM4>
F:218-239/Domain: transmembrane #status predicted <TM5>
F:260-280/Domain: transmembrane #status predicted <TM6>
F:301-320/Domain: transmembrane #status predicted <TM7>
F:28,37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.3%; Score 18; DB 2; Length 404;
Best Local Similarity 28.6%; Pred. No. 8.2e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 349 CASSSSC 355

RESULT 9
T24196
hypothetical protein R11H6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24196
R:Bardill, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19852
A:Accession: T24196
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-442 <WIL>
A:Cross-references: UNIPROT:O45719; EMBL:Z93386; PIDN:CAB07645.1; GSPDB:GN00023; CESP:R1
A:Experimental source: clone R11H6
C:Genetics:
A:Gene: CESP:R11H6.2
A:Map position: 5
A:Introns: 13/3; 68/3; 154/1; 284/1; 356/1

Query Match 33.3%; Score 18; DB 2; Length 442;
Best Local Similarity 28.6%; Pred. No. 8.6e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 10 CAASAC 16

RESULT 10
S49147
ERF-2 protein - human
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49147; I37372
R:Nie, X.F.; Maclean, R.N.; Kumar, V.; McKay, I.A.; Bustin, S.A.
submitted to the EMBL Data Library, April 1994
A:Reference number: S49147
A:Accession: S49147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-492 <NIE>
A:Cross-references: UNIPROT:P47974

C>Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: J05784
R:Haenze, J.; Dittlich, K.; Doetsch, J.; Rascher, W.
Biochem. Biophys. Res. Commun. 240, 183-188, 1997
A:Title: Molecular cloning of a novel human receptor gene with homology to the rat adreno-
A:Reference number: J05784; MUID:98042541; PMID:9367907
A:Accession: J05784
A:Molecule type: mRNA
A:Residues: 1-404 <HAE>
A:Cross-references: UNIPROT:O15218; GB:Y13583; NID:g2652933; PIDN:CAA73910.1; PID:g26529
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; receptor; transmembrane protein
F:58-79/Domain: transmembrane #status predicted <TM1>
F:91-113/Domain: transmembrane #status predicted <TM2>
F:128-149/Domain: transmembrane #status predicted <TM3>
F:171-193/Domain: transmembrane #status predicted <TM4>
F:218-239/Domain: transmembrane #status predicted <TM5>
F:260-280/Domain: transmembrane #status predicted <TM6>
F:301-320/Domain: transmembrane #status predicted <TM7>
F:28,37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.3%; Score 18; DB 2; Length 404;
Best Local Similarity 28.6%; Pred. No. 8.2e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 349 CASSSSC 355

RESULT 9
T24196
hypothetical protein R11H6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24196
R:Bardill, S.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19852
A:Accession: T24196
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-442 <WIL>
A:Cross-references: UNIPROT:O45719; EMBL:Z93386; PIDN:CAB07645.1; GSPDB:GN00023; CESP:R1
A:Experimental source: clone R11H6
C:Genetics:
A:Gene: CESP:R11H6.2
A:Map position: 5
A:Introns: 13/3; 68/3; 154/1; 284/1; 356/1

Query Match 33.3%; Score 18; DB 2; Length 442;
Best Local Similarity 28.6%; Pred. No. 8.6e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 10 CAASAC 16

RESULT 10
S49147
ERF-2 protein - human
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49147; I37372
R:Nie, X.F.; Maclean, R.N.; Kumar, V.; McKay, I.A.; Bustin, S.A.
submitted to the EMBL Data Library, April 1994
A:Reference number: S49147
A:Accession: S49147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-492 <NIE>
A:Cross-references: UNIPROT:P47974

R:Nie, X.F.; Maclean, K.N.; Kumar, V.; McKay, I.A.; Bustin, S.A.
Gene 152, 285-286, 1995
A:Title: ERF-2, the human homologue of the murine Tis11d early response gene.
A:Reference number: I37372; MUID:95137407; PMID:7835719
A:Accession: I37372
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-492 <RES>
A:Cross-references: EMBL:X78992; NID:g509777; PIDN:CAA55592.1; PID:g509778
C:Genetics:
A:Gene: GDB:BRF2; ERF2
A:Cross-references: GDB:511261
A:Map position: I3q12.3-I3q12.3

Query Match 33.3%; Score 18; DB 2; Length 492;
Best Local Similarity 28.6%; Pred. No. 9e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 293 CSSASSC 299

RESULT 11
JC7366
Jun a 2 protein - mountain cedar
C:Species: Juniperus ashei (mountain cedar)
C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:Accession: JC7366; PC7093
R:Yokoyama, M.; Miyahara, M.; Shimizu, K.; Kino, K.; Tsunoo, H.
Biochem. Biophys. Res. Commun. 275, 195-202, 2000
A:Title: Purification, identification, and cDNA cloning of Jun a 2, the second major all.
A:Reference number: JC7366
A:Accession: JC7366
A:Molecule type: mRNA
A:Residues: 1-507 <YOK>
A:Cross-references: UNIPROT:Q9FY19; GB:AJ404653
A:Accession: PC7093
A:Molecule type: protein
A:Residues: 55-63 <Y02>
C:Comment: This protein, a second major allergen of mountain cedar pollen, which is invo
o the polygalacturonase family.
C:Keywords: glycoprotein; pollen

Query Match 33.3%; Score 18; DB 2; Length 507;
Best Local Similarity 28.6%; Pred. No. 9.1e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
Db 348 CTSAAAC 354

RESULT 12
S48730
Cry j II protein - Japanese cedar
C:Species: Cryptomeria japonica (Japanese cedar)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S48730
R:Namba, M.; Kurose, M.; Torigoe, K.; Hino, K.; Taniguchi, Y.; Fukuda, S.; Usui, M.; Ku
FEBS Lett. 353, 124-128, 1994
A:Title: Molecular cloning of the second major allergen, Cry j II, from Japanese cedar
A:Reference number: S48730; MUID:95010777; PMID:7926035
A:Accession: S48730
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <NAM>
A:Cross-references: UNIPROT:P43212; GB:D37765; NID:g577695; PIDN:BAA07021.1; PID:dl0075

Query Match 33.3%; Score 18; DB 2; Length 514;
Best Local Similarity 28.6%; Pred. No. 9.2e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      3 CXXXXXC 9
DB      347 CTSASAC 353

RESULT 13
JC2498
second major allergen Cry j II precursor - Japanese cedar
C:Species: Cryptomeria japonica (Japanese cedar)
C>Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: JC2498; PC2346; A60147
R:Komiyama, N.; Sone, T.; Shimizu, K.; Morikubo, K.; Kino, K.
Biochem. Biophys. Res. Commun. 201, 1021-1028, 1994
A:Title: cDNA cloning and expression of Cry j II, the second major allergen of Japanese
A:Reference number: JC2498; MUID:94271186; PMID:8002372
A:Accession: JC2498
A:Molecule type: mRNA
A:Residues: 1-514 <KOM>
A:Cross-references: UNIPROT:P43212; DBJ:D29772; NID:G506857; PIDN:BAA06172.1; PID:G5068
A:Accession: PC2346
A:Molecule type: protein
A:Residues: 52-61 <KO2>
R:Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui, M.; Matuhasi, T.
Allergy 45, 309-312, 1990
A:Title: Identification of the second major allergen of Japanese cedar pollen.
A:Reference number: A60147; MUID:90342988; PMID:2382797
A:Accession: A60147
A:Molecule type: protein
A:Residues: 55-64 <SAK>
C:Keywords: glycoprotein; pollen
F:1-54/Domain: signal sequence #status predicted <SIG>
F:55-460/Product: second major allergen Cry j #status predicted <MAT>
F:429,460,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      33.3%; Score 18; DB 2; Length 514;
Best Local Similarity 28.6%; Pred. No. 9.2e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      347 CTSASAC 353

RESULT 14
JC7100
polycalacturonase Cha o 2 - Japanese cypress
C:Species: Chamaecyparis obtusa (Japanese cypress)
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: JC7100; PC7026
R:Mori, T.; Yokoyama, M.; Komiyama, N.; Okano, M.; Kino, K.
Biochem. Biophys. Res. Commun. 263, 166-171, 1999
A:Title: Purification, identification, and cDNA cloning of Cha o 2, the second major all
A:Reference number: JC7100; MUID:99417540; PMID:10486272
A:Accession: JC7100
A:Molecule type: mRNA
A:Residues: 1-514 <MOR>
A:Cross-references: UNIPROT:Q7M1E7
A:Accession: PC7026
A:Molecule type: protein
A:Residues: 51-62 <MO2>

Query Match      33.3%; Score 18; DB 2; Length 514;
Best Local Similarity 28.6%; Pred. No. 9.2e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      347 CTSASAC 353

RESULT 15
cdc25A - rat

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C:Species: Rattus sp. (rat)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 22-Jun-1999
C:Accession: I53194
R:Jinno, S.; Suto, K.; Nagata, A.; Igarashi, M.; Kanaoka, Y.; Nojima, H.; Okayama, H.
EMBO J. 13, 1549-1556, 1994
A:Title: Cdc25A is a novel phosphatase functioning early in the cell cycle.
A:Reference number: I53194; MUID:94208523; PMID:8156993
A:Accession: I53194
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-525 <RES>
A:Cross-references: GB:D16236; NID:G484291; PIDN:BAA03761.1; PID:G1008041
C:Superfamily: human protein-tyrosine-phosphatase cdc25A; cdc25-type protein-tyrosine-ph
F:314-507/Domain: cdc25-type protein-tyrosine-phosphatase homology <PTP>

Query Match      33.3%; Score 18; DB 2; Length 525;
Best Local Similarity 28.6%; Pred. No. 9.2e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3 CXXXXXC 9
DB      266 CSSTSSC 272

RESULT 16
CB8UA
complement C8 alpha chain precursor [validated] - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C:Accession: I37213; A26704
R:Michelotti, G.A.; Snider, J.V.; Sodetz, J.M.
Hum. Genet. 95, 513-518, 1995
A:Title: Genomic organization of human complement protein C8 alpha and further examinatio
A:Reference number: I37213; MUID:95278905; PMID:7759071
A:Accession: I37213
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-584 <MIC>
R:Rao, A.G.; Howard, O.M.Z.; Ng, S.C.; Whitehead, A.S.; Colten, H.R.; Sodetz, J.M.
Biochemistry 26, 3556-3564, 1987
A:Title: Complementary DNA and derived amino acid sequence of the alpha subunit of human
A:Reference number: A26704; MUID:88000560; PMID:2820471
A:Accession: A26704
A:Molecule type: mRNA
A:Residues: 1-92,'Q',94-466,'CCGTQAWASGQ',480-574,'P',576-584 <RAO>
A:Note: part of the sequence was confirmed by protein sequencing
R:Hotsteenge, J.; Blommestein, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O.
J. Biol. Chem. 274, 32786-32794, 1999
A:Title: The four terminal components of the complement system are C-mannosylated on mul
A:Reference number: A59362; MUID:20020247; PMID:10551839
A:Contents: annotation
A:Note: identification and location of C-mannosylation sites by mass-spectroscopy
C:Genetics:
A:Gene: GDB:C8A
A:Cross-references: GDB:119735; OMIM:120950
A:Map position: lp32-lp32
A:Introns: 26/2, 57/3, 106/1, 155/2, 218/3, 285/3, 366/1, 408/1, 460/3, 535/1
C:Complex: heterotrimer of C8 alpha chain (PIR:CB8UA), C8 beta chain (PIR:CB8UB), and C8
C:Function:
A:Description: combines with complement C5b-7 complex to polymerize complement component
A:Pathway: complement pathway
C:Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology;
C:Keywords: complement pathway; cytolysis; glycoprotein; membrane attack complex; plasma
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-30/Domain: propeptide #status predicted <PRO>
F:31-584/Product: complement C8 alpha chain #status predicted <MPT>
F:37-91/Domain: thrombospondin type 1 repeat homology <THR1>
F:96-130/Domain: LDL receptor ligand-binding repeat homology <LDL>
F:497-528/Domain: EGF homology <EGF>
F:538-584/Domain: thrombospondin type 1 repeat homology <THR2>
F:43/Binding site: carbohydrate (Asn) (covalent) #status absent
F:44,542,545,548/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental

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F;437/Binding site: carbohydrate (Asn) (covalent): #status predicted

Query Match 33.3%; Score 18; DB 1; Length 584;
Best Local Similarity 28.6%; Pred. No. 9.7e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 84 CSSSTTC 90

RESULT 17

D48492
kpsc protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: D48492; I67694; S36652
R:Pazzani, C.; Rosenow, C.; Boulnois, G.J.; Bronner, D.; Jann, K.; Roberts, I.S.
J. Bacteriol. 175, 5978-5983, 1993
A:Title: Molecular analysis of region 1 of the Escherichia coli K5 antigen gene cluster:
A:Reference number: A48492; MUID:93388530; PMID:8397187
A:Accession: D48492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-675 <PAZ>
A:Cross-references: UNIPROT:P42217; EMBL:X74567; NID:G397404; PIDN:CAA52658.1; PID:G3974
R:Rosenow, C.; Roberts, I.S.; Jann, K.
FEMS Microbiol. Lett. 125, 159-164, 1995
A:Title: Isolation from recombinant Escherichia coli and characterization of CWP-Kdo syn
A:Reference number: I53591; MUID:95180691; PMID:7875563
A:Accession: I67694
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: GB:S76943; NID:G913365

Query Match 33.3%; Score 18; DB 2; Length 675;
Best Local Similarity 28.6%; Pred. No. 1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 361 CTAASAC 367

RESULT 18

T24978
hypothetical protein T19B10.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24978
R:Lennard, N.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19964
A:Accession: T24978
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-746 <WIL>
A:Cross-references: UNIPROT:Q27526; EMBL:Z74043; PIDN:CAA98542.1; GSPDB:GN000023; CESP:T1
A:Experimental source: clone T19B10
C:Genetics:
A:Gene: CESP:T19B10.3
A:Map position: 5
A:Introns: 130/2; 198/2; 227/1; 257/2; 324/1; 479/2; 532/3; 605/3

Query Match 33.3%; Score 18; DB 2; Length 746;
Best Local Similarity 28.6%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 727 CTSSTSC 733

RESULT 19

T34249
hypothetical protein F31D5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34249
R:Wilcox, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F31D5.
A:Reference number: Z21494
A:Accession: T34249
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1817 <WIL>
A:Cross-references: UNIPROT:Q19331; EMBL:U28941; PIDN:AAC71101.1; GSPDB:GN000020; CESP:F3
A:Experimental source: strain Bristol N2; clone F31D5
C:Genetics:
A:Gene: CESP:F31D5.5
A:Map position: 2
A:Introns: 22/2; 107/2; 199/2; 291/2; 384/2; 476/2; 566/2; 648/2; 728/2; 904/2; 1047/2;

Query Match 33.3%; Score 18; DB 2; Length 1817;
Best Local Similarity 28.6%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 448 CTTTTTC 454

RESULT 20

SMNR
metallothionein - cultivated mushroom
C:Species: Agaricus bisporus (cultivated mushroom)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A03286
R:Munger, K.; Lerch, K.
Biochemistry 24, 6751-6756, 1985
A:Title: Copper metallothionein from the fungus Agaricus bisporus: chemical and spectrosc
A:Reference number: A03286
A:Accession: A03286
A:Molecule type: protein
A:Residues: 1-25 <MUN>
A:Cross-references: UNIPROT:P04358
A:Experimental source: mycelium; strain A-32
C:Comment: In contrast to the vertebrate metallothioneins, the fungal proteins bind copp
C:Comment: The absorptive, luminescent, and stereoptical properties of the copper MT are
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 31.5%; Score 17; DB 1; Length 25;
Best Local Similarity 28.6%; Pred. No. 4.4e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 5 CSGASSC 11

RESULT 21

SMNC
metallothionein - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 31-May-1980 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C:Accession: A24641; A03287
R:Muenzer, K.; Germann, U.A.; Lerch, K.
EMBO J. 4, 2665-2668, 1985
A:Title: Isolation and structural organization of the Neurospora crassa copper metalloth
A:Reference number: A24641; MUID:86030247; PMID:2932331
A:Accession: A24641
A:Molecule type: DNA
A:Residues: 1-26 <MUE>

A;Cross-references: UNIPROT:P02807; GB:X03009; NID:g2986; PIDN:CAA26793.1; PID:g2987
 R;Lerch, K.
 Nature 284, 368-370, 1980
 A;Title: Copper metallothionein, a copper-binding protein from *Neurospora crassa*.
 A;Reference number: A03287; MUID:80143244; PMID:6444697
 A;Accession: A03287
 A;Molecule type: protein
 A;Residues: 2-26 <LER>
 C;Genetics:
 A;Introns: 18/1
 C;Superfamily: metallothionein
 C;Keywords: chelation; metal binding; metal-thiolate cluster
 F;4,6,12,14,18,20,23/Binding site: transition metal ions (Cys) #status experimental

Query Match 31.5%; Score 17; DB 1; Length 26;
 Best Local Similarity 28.6%; Pred. No. 4.5e+02;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
 |
 Db 6 CSGASSC 12

RESULT 22
 S55029
 CAP3 protein - anthracnose fungus (*Colletotrichum gloeosporioides*)
 C;Species: *Glomerella cingulata*, *Colletotrichum gloeosporioides*
 C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 A;Accession: S55029
 R;Hwang, C.S.; Kolattukudy, P.E.
 Mol. Gen. Genet. 247, 282-294, 1995
 A;Title: Isolation and characterization of genes expressed uniquely during appressorium
 A;Reference number: S55029; MUID:95287848; PMID:7770033
 A;Accession: S55029
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-26 <HWA>
 A;Cross-references: UNIPROT:Q99334; EMBL:U18756; NID:g619921; PIDN:AAA77679.1; PID:g6199
 C;Genetics:
 A;Introns: 24/3
 C;Superfamily: metallothionein

Query Match 31.5%; Score 17; DB 2; Length 26;
 Best Local Similarity 28.6%; Pred. No. 4.5e+02;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
 |
 Db 6 CASTGTC 12

RESULT 23
 S42359
 ferredoxin [3Fe-4S] - *Giardia lamblia* (fragment)
 C;Species: *Giardia lamblia*
 C;Date: 07-Oct-1994 #sequence_revision 01-Mar-1996 #text_change 12-Jul-2004
 A;Accession: S42359
 R;Townson, S.M.; Hanson, G.R.; Upcroft, J.A.; Upcroft, P.
 Eur. J. Biochem. 220, 439-446, 1994
 A;Title: A purified ferredoxin from *Giardia duodenalis*.
 A;Reference number: S42359; MUID:94170792; PMID:8125101
 A;Accession: S42359
 A;Molecule type: protein
 A;Residues: 1-27 <TOW>
 A;Note: the source is given as *Giardia duodenalis*
 C;Keywords: 3Fe-4S; iron-sulfur protein; metalloprotein
 F;2-24/Domain: ferredoxin 2[4Fe-4S] homology (fragment) <FER>
 F;9,15/Binding site: 3Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 31.5%; Score 17; DB 2; Length 27;
 Best Local Similarity 28.6%; Pred. No. 4.6e+02;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
 |
 Db 9 CSAAGAC 15

RESULT 24 FFYZ

fulvocin C - *Myxococcus fulvus*
 C;Species: *Myxococcus fulvus*
 C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
 A;Accession: A01810
 R;Tsai, H.; Hirsch, H.J.
 Biochim. Biophys. Acta 667, 213-217, 1981
 A;Title: The primary structure of fulvocin C from *Myxococcus fulvus*.
 A;Reference number: A01810; MUID:81161107; PMID:6783114
 A;Accession: A01810
 A;Molecule type: protein
 A;Residues: 1-45 <TSA>
 A;Cross-references: UNIPROT:P01547
 C;Comment: Fulvocin C is a bacteriocin.
 C;Comment: *Myxococcus fulvus* is a myxobacterium; these obligate aerobes are unicellular,
 C;Superfamily: fulvocin C
 C;Keywords: antibacterial

Query Match 31.5%; Score 17; DB 1; Length 45;
 Best Local Similarity 28.6%; Pred. No. 5.8e+02;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
 |
 Db 18 CTTGTAC 24

RESULT 25 AC3539

hypothetical protein BMII0237 [imported] - *Brucella melitensis* (strain 16M)
 C;Species: *Brucella melitensis*
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 A;Accession: AC3539
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
 Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesche
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AC3539
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-45 <KUR>
 A;Cross-references: UNIPROT:Q8YDE0; GB:AE008918; PIDN:AAL53478.1; PID:g17984380; GSPDB:
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BMII0237
 A;Map position: II

Query Match 31.5%; Score 17; DB 2; Length 45;
 Best Local Similarity 28.6%; Pred. No. 5.8e+02;
 Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
 |
 Db 22 CATSSQC 28

RESULT 26 SMHYIC

metallothionein I - Chinese hamster
 C;Species: *Cricetulus griseus* (Chinese hamster)
 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
 A;Accession: A03282; S13737; S50198
 R;Griffith, B.B.; Walters, R.A.; Enger, M.D.; Hildebrand, C.E.; Griffith, J.K.
 Nucleic Acids Res. 11, 901-910, 1983
 A;Title: cDNA cloning and nucleotide sequence comparison of Chinese hamster metallothior
 A;Reference number: A93501; MUID:83168910; PMID:6687636

A;Reference number: S59621; MUID:96067616; PMID:7487956
A;Accession: S59621
A;Molecule type: protein
A;Residues: 1-66 <BER>
A;Cross-references: UNIPROT:P55946
A;Superfamily: metallothionein
C;Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 31.5%; Score 17; DB 2; Length 66;
Best Local Similarity 28.6%; Pred. No. 6.9e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 51 CTGAASC 57

RESULT 29
H95299
hypothetical protein Sma0580 [imported] - Sinorhizobium meliloti (strain 1021) magapla
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95299
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: H95299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <KUR>
A;Cross-references: UNIPROT:Q92Z24; GB:AEO06469; PIDN:AAK64962.1; PID:g14523387; GSPDB:(
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.K.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma0580
A;Genome: plasmid

Query Match 31.5%; Score 17; DB 2; Length 71;
Best Local Similarity 28.6%; Pred. No. 7.1e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 31 CSRTAC 37

RESULT 30
D44007
aptotoxin IV - trap-door spider (Aptostichus schlingeri)
N;Alternate names: insecticidal peptide Aps IV
C;Species: Aptostichus schlingeri
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D44007
R;Skinner, W.S.; Dennis, P.A.; Li, J.P.; Quistad, G.B.
Toxicon 30, 1043-1050, 1992
A;Title: Identification of insecticidal peptides from venom of the trap-door spider, Ap
A;Reference number: A44007; MUID:93069259; PMID:1440641
A;Accession: D44007
A;Molecule type: protein
A;Residues: 1-76 <SKI>
A;Cross-references: UNIPROT:P49269; PIDN:AA24050.1; PID:g259280
A;Note: sequence extracted from NCBI backbone (NCBIP:119527)

A;Accession: A03282
A;Molecule type: mRNA
A;Residues: 1-61 <GRI>
A;Cross-references: UNIPROT:P02804; GB:J00061; NID:g191135; PIDN:AAA36996.1; PID:g304522
R;Grady, D.L.; Robinson, D.L.; Hildebrand, C.E.
Nucleic Acids Res. 18, 7149, 1990
A;Title: Genomic sequence of the Chinese hamster MT I gene.
A;Reference number: S13737; MUID:91088310; PMID:2263484
A;Accession: S13737
A;Molecule type: DNA
A;Residues: 1-61 <GRA>
A;Cross-references: EMBL:X55064; NID:g49468; PIDN:CAA38897.1; PID:g49469
R;Yamada, K.; Kato, H.; Kanda, N.; Fujii-Kuriyama, Y.; Utakoji, T.; Itoh, R.
Biochim. Biophys. Acta 1219, 581-591, 1994
A;Title: Sequence homology of Chinese hamster metallothionein genes I and II to those of
A;Reference number: S50198; MUID:95035087; PMID:7948015
A;Accession: S50198
A;Molecule type: DNA
A;Residues: 1-61 <YAM>
A;Cross-references: GB:D10551; GB:D90509; NID:g633055; PIDN:BAA01408.1; PID:g633056
C;Genetics:
A;Gene: MT-I
A;Introns: 10/1; 32/1
A;Superfamily: metallothionein
C;Keywords: metal binding
F;5,7,13,15,19,21,24,26,29/Binding site: transition metal ions (Cys) #status predicted
F;33,34,36,37,41,44,48,50,57,59,60/Binding site: transition metal ions (Cys) #status pre

Query Match 31.5%; Score 17; DB 1; Length 61;
Best Local Similarity 28.6%; Pred. No. 6.6e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 7 CSTGSTC 13

RESULT 27
S00810
metallothionein Ic - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S00810
R;Peterson, M.G.; Hannan, F.; Mercer, J.F.B.
Eur. J. Biochem. 174, 417-424, 1988
A;Title: The sheep metallothionein gene family. Structure, sequence and evolutionary rel
A;Reference number: S00808; MUID:88254812; PMID:3383853
A;Accession: S00810
A;Molecule type: DNA
A;Residues: 1-61 <PET>
A;Cross-references: UNIPROT:P09578; EMBL:X07974; NID:g1340; PIDN:CAA30786.1; PID:g1341
C;Genetics:
A;Introns: 10/1; 32/1
C;Superfamily: metallothionein

Query Match 31.5%; Score 17; DB 2; Length 61;
Best Local Similarity 28.6%; Pred. No. 6.6e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 CXXXXXC 9
DB 7 CSTGSSC 13

RESULT 28
S59621
metallothionein isoform b, cadmium-binding - Ariantha arbustorum (terrestrial snail)
C;Species: Ariantha arbustorum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S59621
R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Biochem. J. 311, 951-957, 1995
A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion

C:Keywords: disulfide bond; toxin; venom

Query Match 31.5%; Score 17; DB 2; Length 76;
Best Local Similarity 28.6%; Pred. No. 7.3e+02;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CXXXXC 9
Db 30 CSSSSEC 36

Search completed: April 27, 2005, 16:45:12
Job time : 45 secs

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